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Entry information

Entry name	PTMA_CAMCO
Primary accession number	Q45983
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 36, July 1998
Sequence was last modified in	Release 36, July 1998
Annotations were last modified in	Release 44, July 2004

Name and origin of the protein

Protein name	Posttranslational flagellin modification protein A
Synonyms	None
Gene name	Name: ptmA
From	Campylobacter coli [TaxID: 195]
Taxonomy	Bacteria ; Proteobacteria ; Epsilonproteobacteria ; Campylobacterales ; Campylobacteraceae ; Campylobacter .

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=VC167;

MEDLINE=96423180;PubMed=8825781 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]

[Guerry P.](#), [Doig P.](#), [Alm R.A.](#), [Burr D.H.](#), [Kinsella N.](#), [Trust T.J.](#);

"Identification and characterization of genes required for post-translational modification of *Campylobacter coli* VC167 flagellin.";

Mol. Microbiol. 19:369-378(1996).

Comments

- **FUNCTION:** Required for biosynthesis of LAH modification in the post-translational modification of *Campylobacter coli* flagellin.
- **SIMILARITY:** Belongs to the short-chain dehydrogenases/reductases (SDR) family.

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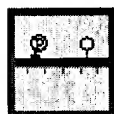
Cross-references

EMBL AY102621; AAM76282.1; -. [[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]
 PIR S70686; S70686.
[IPR002198](#); ADH_short.
 InterPro [IPR002347](#); Adh_short_C2.
[Graphical view of domain structure.](#)
 Pfam [PF00106](#); adh_short; 1.
[Pfam graphical view of domain structure.](#)
 PRINTS [PR00081](#); GDHRDH.
 PROSITE [PS00061](#); ADH_SHORT; FALSE_NEG.
 ProDom [\[Domain structure / List of seq. sharing at least 1 domain\]](#)
 HOBACGEN [\[Family / Alignment / Tree\]](#)
 BLOCKS [Q45983](#).
 ProtoNet [Q45983](#).
 ProtoMap [Q45983](#).
 PRESAGE [Q45983](#).
 DIP [Q45983](#).
 ModBase [Q45983](#).
 SMR [Q45983](#); 46045E806390D69F.
 SWISS-2DPAGE [Get region on 2D PAGE](#).
 UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

Oxidoreductase.

Features



[Feature table viewer](#)

Key	From	To	Length	Description
ACT_SITE	168	168		By similarity.

Sequence information

Length: **256** Molecular weight: **28489** CRC64: **46045E806390D69F** [This is a checksum on the
 AA Da sequence]

10	20	30	40	50	60
MLENKIIFVA	GACGRIGKAL	CKKILQNKGI	AILADINENH	LSILKTELEN	EFKKELLSLR
70	80	90	100	110	120
LDITSKESLN	CAIDQAFEKY	SKIDGFVNSS	YPVGKDWGKI	AYYEASYEQI	CESLNLHLGG
130	140	150	160	170	180
FILASQEFVK	FFKKQSYGNI	INLSSIMGVF	APKFENYENT	TMQSSLEYSV	IKAGINHLGA
190	200	210	220	230	240
WLAKELFNTN	IRVNTLASGG	ILDNQANIFL	EKYRKCCASK	GMLDAEDICG	TLVFLLSDES

250
|
KFVTGQTLVV DDGWGL

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Entry information

Entry name	FLAA_CAMCO
Primary accession number	P27053
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 23, August 1992
Sequence was last modified in	Release 34, October 1996
Annotations were last modified in	Release 44, July 2004
Name and origin of the protein	
Protein name	Flagellin A
Synonyms	None
Gene name	Name: flaA
From	Campylobacter coli [TaxID: 195]
Taxonomy	Bacteria ; Proteobacteria ; Epsilonproteobacteria ; Campylobacterales ; Campylobacteraceae ; Campylobacter .

References

- [1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=VC167 T2;
 MEDLINE=91310584;PubMed=1856171 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
[Guerry P.](#), [Alm R.A.](#), [Power M.E.](#), [Logan S.M.](#), [Trust T.J.](#);
 "Role of two flagellin genes in Campylobacter motility."
[J. Bacteriol.](#) 173:4757-4764(1991).

Comments

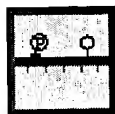
- **FUNCTION:** Flagellin is the subunit protein which polymerizes to form the filaments of bacterial flagella.
- **SUBUNIT:** Heteropolymer of flaA and flaB. A flagellar filament composed exclusively of flaA is indistinguishable in length from that of the wild type and shows a slight reduction in motility. The flagellar filament composed exclusively of the flaB is severely truncated in length and greatly reduced in motility. Thus, while both flagellins are not necessary for motility, both are required for a fully active flagellar filament.
- **SIMILARITY:** Belongs to the bacterial flagellin family.

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Cross-references

EMBL M64670; AAA23022.1; -. [[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]
M64671; AAA23026.1; -. [[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]
PIR [A42474](#); [A42474](#).
HSSP [P06179](#); 1UCU. [[HSSP ENTRY](#) / [PDB](#)]
InterPro [IPR001029](#); Flagellin_C.
[IPR010810](#); Flagellin_IN.
[IPR001492](#); Flagellin_N.
[Graphical view of domain structure.](#)
Pfam [PF00700](#); Flagellin_C; 1.
[PF07196](#); Flagellin_IN; 2.
[PF00669](#); Flagellin_N; 1.
[Pfam graphical view of domain structure.](#)
PRINTS [PR00207](#); FLAGELLIN.
ProDom [PD000316](#); Flagellin_C; 2.
[\[Domain structure / List of seq. sharing at least 1 domain\]](#)
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ProtoMap [P27053](#).
PRESAGE [P27053](#).
DIP [P27053](#).
ModBase [P27053](#).
SMR [P27053](#); BD97DFF6CD099004.
SWISS-2DPAGE [Get region on 2D PAGE](#).
UniRef View cluster of proteins with at least [50%](#) / [90%](#) identity.

Keywords**Flagellum.****Features**

Feature table viewer

Key	From	To	Length	Description
INIT_MET	0	0		By similarity.
VARIANT	201	202	2	DS -> QN.

Sequence information

Length: **572** Molecular weight: **58880** CRC64: **BD97DFF6CD099004** [This is a checksum on the sequence]
AA **Da**

10	20	30	40	50	60
GFRINTNVAA	LNAKANSDLN	SRALDQSLSR	LSSGLRINSA	ADDASGMAIA	DSLRSQANTL

```

      70           80           90          100          110          120
      |           |           |           |           |           |
GQAISNGNDA LGILQTADKA MDEQLKILDT IKTKATQAAQ DGQSLKTRTM LQADINRLME

      130          140          150          160          170          180
      |           |           |           |           |           |
ELDNIANTTS FNGKQLLSGG FTNQEFQIGS SSNQTIKASI GATQSSKIGV TRFETGSQSF

      190          200          210          220          230          240
      |           |           |           |           |           |
SSGTVGLTIK NYNGIEDFKF DSVVISTSVG TGLGALAEI NRNADKTGIR ATFDVKSVGA

      250          260          270          280          290          300
      |           |           |           |           |           |
YAIKAGNTSQ DFAINGVVIG KVDYSDGDEI GSLISAINAV KDTTGVQASK DENGKLVLTG

      310          320          330          340          350          360
      |           |           |           |           |           |
ADGRGIKITG SIGVGAGILH TENYGRSLV KNDGRDINIS GTGLSAIGMG ATDMISQSSV

      370          380          390          400          410          420
      |           |           |           |           |           |
SLRESKGQIS AANADAMGFN AYNGGGAQI IFASSIAGFM SQAGSGFSAG SGFSVSGSKN

      430          440          450          460          470          480
      |           |           |           |           |           |
YSAILSASIQ IVSSARSISS TYVVSTGSGF SAGSGNSQFA ALRISTVSAH DETAGVTTLK

      490          500          510          520          530          540
      |           |           |           |           |           |
GAMAVMDIAE TAITNLDQIR ADIGSVQNQI TSTINNITVT QVNVKSAESQ IRDVDFASES

      550          560          570
      |           |           |
ANYSKANILA QSGSYAMAQA NSSQQNVLRL LQ

```

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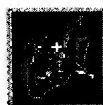
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or at [NCBI \(USA\)](#)




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Entry information

Entry name	O30688
Primary accession number	O30688
Secondary accession numbers	None
Entered in TrEMBL in	Release 05, January 1998
Sequence was last modified in	Release 05, January 1998
Annotations were last modified in	Release 24, June 2003
Name and origin of the protein	
Protein name	Flagellin A [Fragment]
Synonyms	None
Gene name	Name: flaA
From	<u>Campylobacter coli</u> [TaxID: 195]
Taxonomy	<u>Bacteria</u> ; <u>Proteobacteria</u> ; <u>Epsilonproteobacteria</u> ; <u>Campylobacterales</u> ; <u>Campylobacteraceae</u> ; <u>Campylobacter</u> .

References

- [1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=D1159;
Meinersmann R.J., Helsel L.O., Fields P.I., Hiatt K.L.;
 "Discrimination of *Campylobacter jejuni* by fla gene sequencing."
J. Clin. Microbiol. 0:0-0(1997).

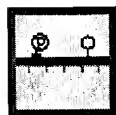
Comments

None

Cross-references

EMBL	AF015091; AAB69353.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] GO:0009420 ; Cellular component: flagellar filament (sensu Bacteria) (<i>inferred from electronic annotation</i>).
GO	GO:0005198 ; Molecular function: structural molecule activity (<i>inferred from electronic annotation</i>). GO:0001539 ; Biological process: ciliary or flagellar motility (<i>inferred from electronic annotation</i>). IPR001492 ; Flagellin_N.

InterPro [Graphical view of domain structure.](#)
 Pfam [PF00669; Flagellin_N; 1.](#)
[Pfam graphical view of domain structure.](#)
 ProtoMap [O30688.](#)
 PRESAGE [O30688.](#)
 ModBase [O30688.](#)
 SMR [O30688; A1EBB1B61699B04D.](#)
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Keywords**Flagellum.****Features**[Feature table viewer](#)

Key	From	To	Length	Description
NON_TER	1	1		
NON_TER	89	89		

Sequence information

Length: **89 AA** [This is the length of the partial sequence]
 Molecular weight: **9630 Da** [This is the MW of the partial sequence]
 CRC64: **A1EBB1B61699B04D** [This is a checksum on the sequence]

10	20	30	40	50	60
QDGQSLKTRT	MLQADINRLM	EELDNIANTT	SFNGKQLLSG	NFINQEFQIG	ASSNQTVKAT
70	80				
IGATQSSKIG	LTRFETGGRI	SSSGEVQFT			

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[Dotlet \(Java\)](#)

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[\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

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Entry information

Entry name	Q9WW79
Primary accession number	Q9WW79
Secondary accession numbers	None
Entered in TrEMBL in	Release 12, November 1999
Sequence was last modified in	Release 12, November 1999
Annotations were last modified in	Release 19, December 2001
Name and origin of the protein	
Protein name	Flagellin A [Fragment]
Synonyms	None
Gene name	Name: flaA
From	<u>Campylobacter coli</u> [TaxID: 195]
Taxonomy	<u>Bacteria</u> ; <u>Proteobacteria</u> ; <u>Epsilonproteobacteria</u> ; <u>Campylobacterales</u> ; <u>Campylobacteraceae</u> ; <u>Campylobacter</u> .

References

- [1] SEQUENCE FROM NUCLEIC ACID.
Studer E., Dohmke M., Wegmueller B., Luethy J., Schmid S., Candrian U.;
"RFLP and sequence analysis of *Campylobacter jejuni* and *Campylobacter coli* PCR products
amplified directly from environmental samples."; Food Sci. Technol. 31:337-345(1998).
- [2] SEQUENCE FROM NUCLEIC ACID.
Studer E.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

Comments

None

Cross-references

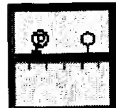
ProtoMap	Q9WW79 .
PRESAGE	Q9WW79 .
ModBase	Q9WW79 .
SMR	Q9WW79 ; C7C0EFB7A1739156.
SWISS-2DPAGE	Get region on 2D PAGE .

UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

Flagellum.

Features



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Key	From	To	Length	Description
NON_TER	1	1		

Sequence information

Length: **14 AA** [This is the length of the partial sequence]

Molecular weight: **1611 Da** [This is the MW of the partial sequence]

CRC64: **C7C0EFB7A1739156** [This is a checksum on the sequence]

10
|
QANSVQQNVL RLLQ

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Entry information

Entry name	Q46009
Primary accession number	Q46009
Secondary accession numbers	None
Entered in TrEMBL in	Release 01, November 1996
Sequence was last modified in	Release 01, November 1996
Annotations were last modified in	Release 26, March 2004
Name and origin of the protein	
Protein name	Flagellin
Synonyms	None
Gene name	None
From	Campylobacter coli [TaxID: 195]
Taxonomy	Bacteria ; Proteobacteria ; Epsilonproteobacteria ; Campylobacterales ; Campylobacteraceae ; Campylobacter .

References

- [1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=VC167;
 MEDLINE=89255058;PubMed=2722741 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
[Logan S.M.](#), [Trust T.J.](#), [Guerry P.](#);
 "Evidence for posttranslational modification and gene duplication of Campylobacter flagellin."
[J. Bacteriol.](#) 171:3031-3038(1989).

Comments

None

Cross-references

EMBL	M26945; AAA23021.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	A44757 ; A44757 . GO:0009420 ; Cellular component: flagellar filament (sensu Bacteria) (<i>inferred from electronic annotation</i>).
GO	GO:0005198 ; Molecular function: structural molecule activity (<i>inferred from electronic annotation</i>). GO:0001539 ; Biological process: ciliary or flagellar motility (<i>inferred from electronic</i>

annotation).

InterPro [IPR001029](#); Flagellin_C.
[IPR010810](#); Flagellin_IN.
[IPR001492](#); Flagellin_N.
[Graphical view of domain structure.](#)

Pfam [PF00700](#); Flagellin_C; 1.
[PF07196](#); Flagellin_IN; 2.
[PF00669](#); Flagellin_N; 1.
[Pfam graphical view of domain structure.](#)

PRINTS [PR00207](#); FLAGELLIN.

ProDom [PD000316](#); Flagellin_C; 1.
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ProtoMap [Q46009](#).

PRESAGE [Q46009](#).

ModBase [Q46009](#).

SMR [Q46009](#); DA7CCBB23588EA7A.

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Keywords**Flagellum.****Features**

None

Sequence information

Length: **572** Molecular weight: **58982** CRC64: **DA7CCBB23588EA7A** [This is a checksum on the
 AA Da sequence]

10	20	30	40	50	60
MGFRINTNVA	ALNAKANSDL	NSRALDQSL	RLSSGLRINS	AADVASGMAI	ADSLRSQANT
70	80	90	100	110	120
LGQAISNGND	ALGILQTADK	AMDEQLKILD	TIKTKATQAA	EDGQSLKTRT	MLQADINRLM
130	140	150	160	170	180
EELDNIANTT	SFNGKQLLSG	GFTNQEFQIG	SSSNQTIKAS	IGATQSSKIG	VTRLNRFTKF
190	200	210	220	230	240
SSGTVGLTIK	NYNGIEDFKF	DSVVISTSVG	TGLGALAEI	NRNADKTGIR	ATFDLKSVGA
250	260	270	280	290	300
YAIKAGNTSQ	DFAINGVVIG	KVDYSDGDEN	GSLISAINAV	KDTTGVQASK	DENGKLVLT
310	320	330	340	350	360
ADGRGIKITG	SIGVGAGILH	TENYGRLSLV	KNDGRDINIS	GTGFSAIMGM	ATDMISQSSV

```

      370          380          390          400          410          420
      |           |           |           |           |           |
SLRESKGQIS AANADAMGFN AYNGGGAKQI IFASSIAGFM SQAGSGFSAG SGFSVGSGKN

      430          440          450          460          470          480
      |           |           |           |           |           |
YSAILSASIQ IVSSAASSIS TYVVSTGSGF SAGSGNSQFA ALRISTVSAH DETAGVTTLK

      490          500          510          520          530          540
      |           |           |           |           |           |
GAMAVMDIAE TAITNLDQIR ADIGSVQNQI TSTINNITVT QVNVKSAESQ IRDVDFASES

      550          560          570
      |           |           |
ANYSKANILA QSGSYAMAQA NSSQQNVLRL LQ

```

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[Dotlet \(Java\)](#)

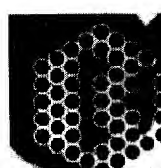


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DATABASE BROWSING

EBI Dbfetch

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DT    23-DEC-2002 (Rel. 74, Last updated, Version 4)
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OC    Campylobacteraceae; Campylobacter.
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RX    PUBMED; 2722741.
RA    Logan S.M., Trust T.J., Guerry P.;
RT    "Evidence for posttranslational modification and gene duplication of
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RL    J. Bacteriol. 171(6):3031-3038(1989).
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XX
SV    M64670.1
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DT    05-JUL-1999 (Rel. 60, Last updated, Version 3)
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OC    Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
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RP    1-4200
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RX    PUBMED; 1856171.
RA    Guerry P., Alm R.A., Power M.E., Logan S.M., Trust T.J.;
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Search in Swiss-Prot and TrEMBL for: coli campylobacter flagellin

Swiss-Prot Release 44.4 of 31-Aug-2004

TrEMBL Release 27.4 of 31-Aug-2004

-
- Number of sequences found in [Swiss-Prot](#)₍₄₎ and [TrEMBL](#)₍₅₎: 9
 - Note that the selected sequences can be saved to a file to be later retrieved; to do so, go to the [bottom](#) of this page.
 - For more directed searches, you can use the Sequence Retrieval System [SRS](#).
-

Search in Swiss-Prot: There are matches to 4 out of 158010 entries

[FLAA_CAMCO \(P27053\)](#)

Flagellin A. {GENE: Name=flaA} - Campylobacter coli

[FLAB_CAMCO \(P18245\)](#)

Flagellin B (Flagellin N). {GENE: Name=flaB} - Campylobacter coli

[PTMA_CAMCO \(Q45983\)](#)

Posttranslational flagellin modification protein A. {GENE: Name=ptmA} - Campylobacter coli

[PTMB_CAMCO \(Q45982\)](#)

Posttranslational flagellin modification protein B. {GENE: Name=ptmB} - Campylobacter coli

Search in TrEMBL: There are matches to 5 out of 1377572 entries

[O30688](#)

Flagellin A (Fragment) {GENE: Name=flaA} - Campylobacter coli

[Q46009](#)

Flagellin - Campylobacter coli

[Q8G9F1](#)

Flagellin (Fragment) {GENE: Name=flaA} - Campylobacter coli

[Q8G9F3](#)

Flagellin (Fragment) {GENE: Name=flaA} - Campylobacter coli

[Q9WW79](#)

Flagellin A (Fragment) {GENE: Name=flaA} - Campylobacter coli

New Search

in Swiss-Prot/TrEMBL by AC, ID, description,
gene name, organism

**Please do NOT use any boolean operators (and,
or, etc.)**

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Format: ☒ Swiss-Prot ☐ Fasta

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or

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If your question is not covered, please contact [<helpdesk@expasy.org>](mailto:helpdesk@expasy.org).

NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402 (1997).

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Query length: 420 AA (of which 5% low-complexity regions filtered out)
Date run: 2004-09-02 16:29:13 UTC+0100 on sib-gml.unil.ch
Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]
Database: EXPASY/UniProt
1,544,870 sequences; 494,584,931 total letters

List of potentially matching sequences

Send selected sequences to

☐ Include query sequence

Db	AC	Description	Score	E-value
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<input type="checkbox"/>	tr Q84IB9	Flagellin (Fragment) [flaA] [Campylobacter jejuni]	736	0.0
<input type="checkbox"/>	tr Q46009	Flagellin [Campylobacter coli]	724	0.0
<input type="checkbox"/>	sp P18245	FLAB_CAMCO Flagellin B (Flagellin N) [flaB] [Campyloba...]	723	0.0
<input type="checkbox"/>	tr Q9RPY6	Flagellin A [flaA] [Campylobacter jejuni]	722	0.0
<input type="checkbox"/>	tr Q99QL6	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	702	0.0
<input type="checkbox"/>	tr Q99Q27	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	696	0.0
<input type="checkbox"/>	tr Q93NL6	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	687	0.0
<input type="checkbox"/>	tr Q93NL9	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	687	0.0
<input type="checkbox"/>	sp P22251	FLA2_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	674	0.0

<input type="checkbox"/>	tr Q8G9F3	Flagellin (Fragment) [flaA] [Campylobacter coli]	674	0.0
<input type="checkbox"/>	tr Q85179	Flagellin A [flaA] [Campylobacter jejuni]	674	0.0
<input type="checkbox"/>	tr Q9R950	Flagellin A [flaA] [Campylobacter jejuni]	672	0.0
<input type="checkbox"/>	tr Q9RF26	Chimeric flagellin A/B [Campylobacter jejuni]	670	0.0
<input type="checkbox"/>	tr Q9R953	Flagellin A [flaA] [Campylobacter jejuni]	669	0.0
<input type="checkbox"/>	tr Q85183	Flagellin A [flaA] [Campylobacter jejuni]	667	0.0
<input type="checkbox"/>	sp P22252	FLB2_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	660	0.0
<input type="checkbox"/>	tr Q9RF25	Flagellin B [flaB] [Campylobacter jejuni]	660	0.0
<input type="checkbox"/>	tr Q7X516	FlaB [flaB] [Campylobacter jejuni]	657	0.0
<input type="checkbox"/>	tr Q6L5K6	Flagellin (Fragment) [flaA] [Campylobacter lari]	608	e-173
<input type="checkbox"/>	tr Q6L5K7	Flagellin (Fragment) [flaA] [Campylobacter lari]	606	e-172
<input type="checkbox"/>	tr Q6L5K1	Flagellin (Fragment) [flaA] [Campylobacter lari]	606	e-172
<input type="checkbox"/>	tr Q6L5J8	Flagellin (Fragment) [flaA] [Campylobacter lari]	604	e-172
<input type="checkbox"/>	tr Q6L5K8	Flagellin (Fragment) [flaA] [Campylobacter lari]	604	e-171
<input type="checkbox"/>	tr Q6L5K2	Flagellin (Fragment) [flaA] [Campylobacter lari]	603	e-171
<input type="checkbox"/>	tr Q6L5K9	Flagellin (Fragment) [flaA] [Campylobacter lari]	602	e-171
<input type="checkbox"/>	tr Q6L5J9	Flagellin (Fragment) [flaA] [Campylobacter lari]	602	e-171
<input type="checkbox"/>	tr Q6L5J6	Flagellin (Fragment) [flaA] [Campylobacter lari]	600	e-170
<input type="checkbox"/>	tr Q6L5K4	Flagellin (Fragment) [flaA] [Campylobacter lari]	600	e-170
<input type="checkbox"/>	tr Q6L5K5	Flagellin (Fragment) [flaA] [Campylobacter lari]	599	e-170
<input type="checkbox"/>	tr Q6L5J7	Flagellin (Fragment) [flaA] [Campylobacter lari]	599	e-170
<input type="checkbox"/>	tr Q6L5L1	Flagellin (Fragment) [flaA] [Campylobacter lari]	598	e-170
<input type="checkbox"/>	tr Q6L5L0	Flagellin (Fragment) [flaA] [Campylobacter lari]	598	e-170
<input type="checkbox"/>	tr Q6L5K0	Flagellin (Fragment) [flaA] [Campylobacter lari]	598	e-170
<input type="checkbox"/>	sp Q46113	FLA3_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	597	e-169
<input type="checkbox"/>	tr Q85180	Flagellin A [flaA] [Campylobacter jejuni]	590	e-167
<input type="checkbox"/>	tr Q84IB8	Flagellin (Fragment) [flaA] [Campylobacter jejuni]	590	e-167
<input type="checkbox"/>	tr Q6L5K3	Flagellin (Fragment) [flaA] [Campylobacter lari]	590	e-167
<input type="checkbox"/>	tr Q9R952	Flagellin A [flaA] [Campylobacter jejuni]	589	e-167
<input type="checkbox"/>	tr Q30696	Flagellin A [flaA] [Campylobacter jejuni]	588	e-167
<input type="checkbox"/>	tr Q8G9F1	Flagellin (Fragment) [flaA] [Campylobacter coli]	588	e-167
<input type="checkbox"/>	tr Q85182	Flagellin A [flaA] [Campylobacter jejuni]	586	e-166
<input type="checkbox"/>	tr Q9R949	Flagellin A [flaA] [Campylobacter jejuni]	586	e-166
<input type="checkbox"/>	tr Q34938	Flagellin A [flaA] [Campylobacter jejuni]	585	e-166
<input type="checkbox"/>	sp P56963	FLA1_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	585	e-166
<input type="checkbox"/>	tr Q8G9F2	Flagellin (Fragment) [flaA] [Campylobacter jejuni]	584	e-166
<input type="checkbox"/>	tr Q30689	Flagellin A [flaA] [Campylobacter jejuni]	583	e-165
<input type="checkbox"/>	sp Q46114	FLB3_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	581	e-165
<input type="checkbox"/>	tr Q8G9F0	Flagellin (Fragment) [flaA] [Campylobacter jejuni]	578	e-164
<input type="checkbox"/>	tr Q93NL8	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	572	e-162
<input type="checkbox"/>	tr Q79AR6	Flagellin [flaA] [Campylobacter jejuni]	572	e-162
<input type="checkbox"/>	tr Q933V4	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	570	e-161
<input type="checkbox"/>	tr Q85181	Flagellin B [flaB] [Campylobacter jejuni]	570	e-161
<input type="checkbox"/>	tr Q93NL7	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	569	e-161
<input type="checkbox"/>	sp P56964	FLB1_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	566	e-160

<input type="checkbox"/>	tr Q9R954	Flagellin B [flaB] [Campylobacter jejuni]	565	e-160
<input type="checkbox"/>	tr Q9R951	Flagellin B [flaB] [Campylobacter jejuni]	564	e-160
<input type="checkbox"/>	tr P96751	Flagellin (Fragment) [flaA] [Campylobacter sp]	561	e-159
<input type="checkbox"/>	tr P96752	Flagellin [flaB] [Campylobacter sp]	559	e-158
<input type="checkbox"/>	tr Q93GT4	Flagellin (Fragment) [flaA] [Campylobacter lari]	489	e-137
<input type="checkbox"/>	tr Q93R24	Flagellin (Fragment) [flaA] [Campylobacter lari]	488	e-137
<input type="checkbox"/>	tr Q84IC8	Flagellin (Fragment) [flaA] [Campylobacter lari]	483	e-135
<input type="checkbox"/>	tr Q84IC3	Flagellin (Fragment) [flaA] [Campylobacter lari]	482	e-135
<input type="checkbox"/>	tr Q84IC6	Flagellin (Fragment) [flaA] [Campylobacter lari]	481	e-135
<input type="checkbox"/>	tr Q84IC5	Flagellin (Fragment) [flaA] [Campylobacter lari]	481	e-135
<input type="checkbox"/>	tr Q84IC4	Flagellin (Fragment) [flaA] [Campylobacter lari]	481	e-135
<input type="checkbox"/>	tr Q8RTY4	Flagellin (Fragment) [flaA] [Campylobacter lari]	479	e-134
<input type="checkbox"/>	tr Q84IC9	Flagellin (Fragment) [flaA] [Campylobacter lari]	479	e-134
<input type="checkbox"/>	tr Q93GT1	Flagellin (Fragment) [flaA] [Campylobacter lari]	478	e-134
<input type="checkbox"/>	tr Q84IC7	Flagellin (Fragment) [flaA] [Campylobacter lari]	478	e-133
<input type="checkbox"/>	tr Q84IC1	Flagellin (Fragment) [flaA] [Campylobacter lari]	473	e-132
<input type="checkbox"/>	tr Q93GT2	Flagellin (Fragment) [flaA] [Campylobacter lari]	473	e-132
<input type="checkbox"/>	tr Q84IC2	Flagellin (Fragment) [flaA] [Campylobacter lari]	471	e-131
<input type="checkbox"/>	tr Q93GT3	Flagellin (Fragment) [flaA] [Campylobacter lari]	463	e-129
<input type="checkbox"/>	tr Q46462	Flagellin (Fragment) [fla2] [Campylobacter upsaliensis]	453	e-126
<input type="checkbox"/>	tr Q46461	Flagellin (Fragment) [fla1] [Campylobacter upsaliensis]	444	e-123
<input type="checkbox"/>	tr Q84IC0	Flagellin (Fragment) [flaA] [Campylobacter lari]	424	e-117
<input type="checkbox"/>	tr Q7M7N1	FLAGELLIN B [FLAB] [Wolinella succinogenes]	383	e-105
<input type="checkbox"/>	tr Q7X2D0	Flagellin B [flaB] [Helicobacter pylori (Campylobacter...]	380	e-104
<input type="checkbox"/>	tr Q56746	Flagellin [flag] [Wolinella succinogenes]	379	e-104
<input type="checkbox"/>	sp Q07911	FLAB_HELPY Flagellin B (Flagellin N) [flaB] [Helicobac...]	376	e-103
<input type="checkbox"/>	sp Q9ZMV8	FLAB_HELPJ Flagellin B (Flagellin N) [flaB] [Helicobac...]	376	e-103
<input type="checkbox"/>	tr Q8RNU8	Flagellin B subunit [flaB] [Helicobacter pylori (Campy...]	376	e-103
<input type="checkbox"/>	tr Q6VYQ1	Flagellin B [flaB] [Helicobacter pylori (Campylobacter...]	376	e-103
<input type="checkbox"/>	tr Q8GD49	Flagellin [flaB] [Helicobacter pylori (Campylobacter p...]	375	e-103
<input type="checkbox"/>	sp Q07910	FLAB_HELMU Flagellin B (Flagellin N) [flaB] [Helicobac...]	368	e-100
<input type="checkbox"/>	tr Q7X2D1	Flagellin A [flaA] [Helicobacter pylori (Campylobacter...]	365	e-100
<input type="checkbox"/>	tr Q9XB37	Flagellin B [flaB] [Helicobacter felis]	365	e-100
<input type="checkbox"/>	tr Q7TTM9	Major flagellin subunit FlaA_1 (Major flagellin subuni...]	363	3e-99
<input type="checkbox"/>	sp Q03843	FLAA_HELPY Flagellin A [flaA] [Helicobacter pylori (Ca...]	361	1e-98
<input type="checkbox"/>	sp Q9XB38	FLAA_HELFE Flagellin A [flaA] [Helicobacter felis]	358	1e-97
<input type="checkbox"/>	tr Q6VYQ2	Flagellin A [flaA] [Helicobacter pylori (Campylobacter...]	358	1e-97
<input type="checkbox"/>	tr Q7VF81	Minor flagellin subunit FlaB [flaB] [Helicobacter hepa...]	356	5e-97
<input type="checkbox"/>	sp P50612	FLAA_HELMU Flagellin A [flaA] [Helicobacter mustelae]	345	9e-94
<input type="checkbox"/>	tr Q8VN93	Flagellin B (Fragment) [flaB] [Helicobacter pylori (Ca...]	335	1e-90
<input type="checkbox"/>	tr Q8VN92	Flagellin B (Fragment) [flaB] [Helicobacter pylori (Ca...]	334	2e-90
<input type="checkbox"/>	tr Q93NM0	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	332	8e-90
<input type="checkbox"/>	tr Q93NM1	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	332	1e-89
<input type="checkbox"/>	tr Q8VN91	Flagellin A (Fragment) [flaA] [Helicobacter pylori (Ca...]	330	2e-89
<input type="checkbox"/>	tr Q8VN90	Flagellin A (Fragment) [flaA] [Helicobacter pylori (Ca...]	330	2e-89

Graphical overview of the alignments

[Click here](#)

to resubmit your query after masking regions matching PROSITE profiles
or Pfam HMMs

([?](#) Help) (use ScanProsite for more details about PROSITE matches)

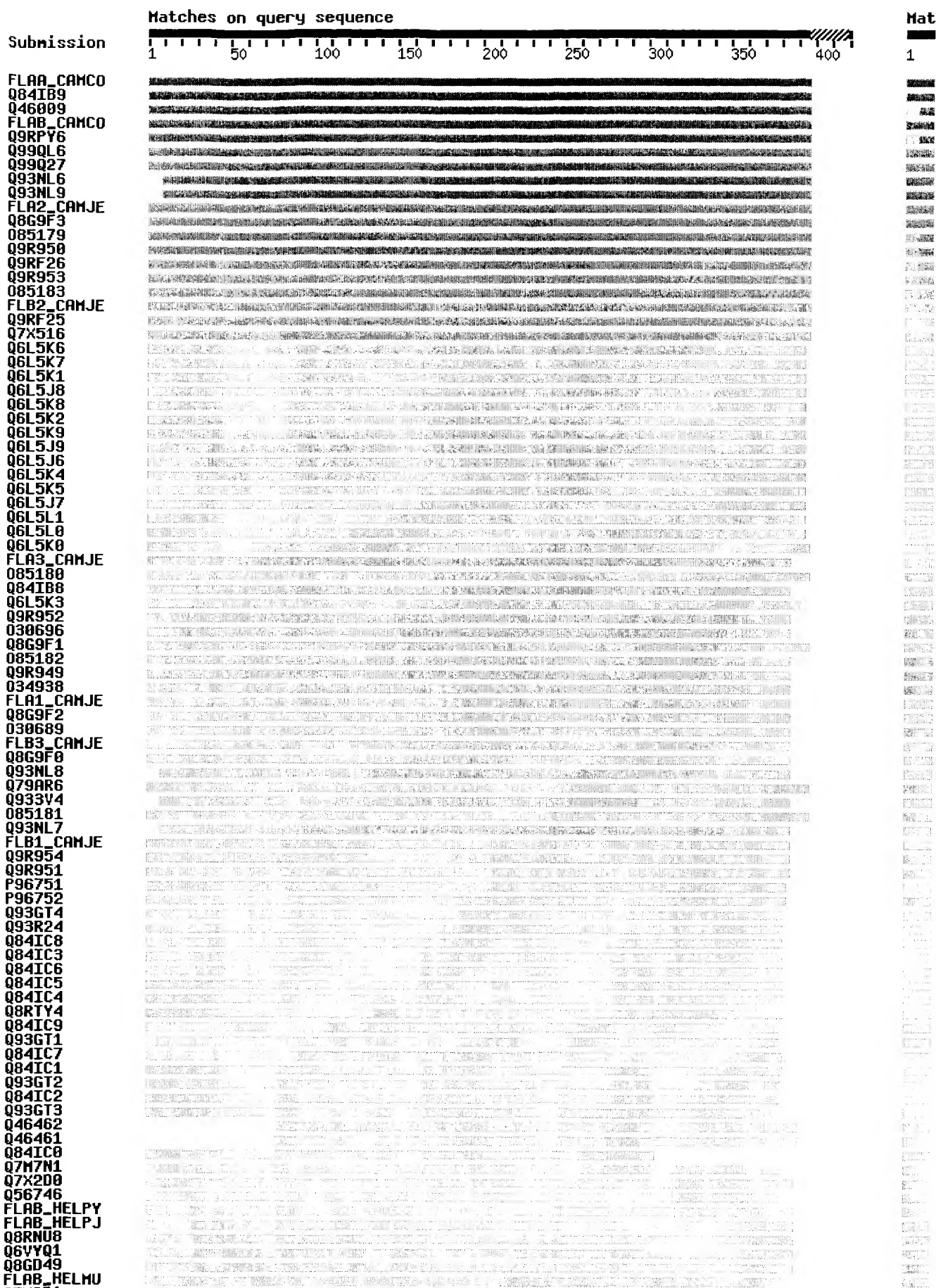
Profile hits

Pfam hits

Flagellin_N

Flagellin_

Flagelli



Alignments

sp P27053 **Flagellin A [flaA] [Campylobacter coli]** 572 AA
FLAA_CAMCO align

Score = 750 bits (1937), Expect = 0.0
Identities = 396/396 (100%), Positives = 396/396 (100%)

Query: 1 GFRINTNVAALNAKANSDLNSRALDQSLSRSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTNVAALNAKANSDLNSRALDQSLSRSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1 GFRINTNVAALNAKANSDLNSRALDQSLSRSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME
Sbjct: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF
Sbjct: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDVKS VGA 240
SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDVKS VGA
Sbjct: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDVKS VGA 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS 300
YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS
Sbjct: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS 300

Query: 301 ADGRGIKITGSIGVGAGILHTENYGRSLVKN DGRDINISGTGLSAIGMGATDMISQSSV 360
ADGRGIKITGSIGVGAGILHTENYGRSLVKN DGRDINISGTGLSAIGMGATDMISQSSV
Sbjct: 301 ADGRGIKITGSIGVGAGILHTENYGRSLVKN DGRDINISGTGLSAIGMGATDMISQSSV 360

Query: 361 SLRESKGQISAANADAMGFNAYNGGGAKQII FASSI 396
SLRESKGQISAANADAMGFNAYNGGGAKQII FASSI
Sbjct: 361 SLRESKGQISAANADAMGFNAYNGGGAKQII FASSI 396

tr Q84IB9 **Flagellin (Fragment) [flaA] [Campylobacter jejuni]** 572 AA
align

Score = 736 bits (1901), Expect = 0.0
Identities = 389/396 (98%), Positives = 392/396 (98%)

Query: 1 GFRINTNVAALNAKANSDLNSRALDQSLSRSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTN AALNAKANSDLNSRALDQSLSRSSGLRINSAADDASGMAIADSLRSQANT+
Sbjct: 1 GFRINTNGAALNAKANSDLNSRALDQSLSRSSGLRINSAADDASGMAIADSLRSQANTM 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
GQAISNG+DALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME
Sbjct: 61 GQAISNGDDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF
Sbjct: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180

```
Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDVKS VGA 240
          SSGTVGLTIKNYNGIEDFKF +VVISTSVGTGLGALAEINRNADKTGIRATFDVKS VGA
Sbjct: 181 SSGTVGLTIKNYNGIEDFKFQNVVISTSVGTGLGALAEINRNADKTGIRATFDVKS VGA 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS 300
          Y IKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS
Sbjct: 241 YTIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS 300

Query: 301 ADGRGIKITGSIGVGAGILHTENYGRSLVKN DGRDINISGTGLSAIGMGATDMISQSSV 360
          ADGRGIKITGSIGVGAGILHTENYGRSLVKN GRDINISGTGLSAIGMGATDMISQSSV
Sbjct: 301 ADGRGIKITGSIGVGAGILHTENYGRSLVKNVGRDINISGTGLSAIGMGATDMISQSSV 360

Query: 361 SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
          SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI
Sbjct: 361 SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
```

```
tr    Q46009          Flagellin [Campylobacter coli]          572 AA
                                align
```

Score = 724 bits (1869), Expect = 0.0
Identities = 385/396 (97%), Positives = 389/396 (98%), Gaps = 1/396 (0%)

```
Query: 1   GFRINTNVAALNAKANSDLNSRALDQSL SRLSSGLRINSAADDASGMAIADSLRSQANTL 60
          GFRINTNVAALNAKANSDLNSRALDQSL SRLSSGLRINSAAD ASGMAIADSLRSQANTL
Sbjct: 2   GFRINTNVAALNAKANSDLNSRALDQSL SRLSSGLRINSAADVASGMAIADSLRSQANTL 61

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
          GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAA+DGQSLKTRTMLQADINRLME
Sbjct: 62  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAEDGQSLKTRTMLQADINRLME 121

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQS F 180
          ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTR ++ F
Sbjct: 122 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRLNRFTK-F 180

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDVKS VGA 240
          SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFD+KSVGA
Sbjct: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDLKSVGA 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS 300
          YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS
Sbjct: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS 300

Query: 301 ADGRGIKITGSIGVGAGILHTENYGRSLVKN DGRDINISGTGLSAIGMGATDMISQSSV 360
          ADGRGIKITGSIGVGAGILHTENYGRSLVKN DGRDINISGTG SAIGMGATDMISQSSV
Sbjct: 301 ADGRGIKITGSIGVGAGILHTENYGRSLVKN DGRDINISGTG FSAIGMGATDMISQSSV 360

Query: 361 SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
          SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI
Sbjct: 361 SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
```

```
sp    P18245          Flagellin B (Flagellin N) [flaB] [Campylobacter coli] 572 AA
      FLAB_CAMCO
                                align
```

tr	Q99QL6	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	574 AA align

9/2/04

Sbjct: 181 TSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEIINKNADKTGVRATYDVKTTGA 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLT 300
YAIKAG TSQDFAINGV+IGKVDY DGD NGSLISAINAVKDTTGVQASKDENGKLVLT

Sbjct: 241 YAIKAGTTSQDFAINGVIIGKVDYKGDNNGSLISAINAVKDTTGVQASKDENGKLVLT 300

Query: 301 ADGRGIKITGSIGVGAGILHT--ENYGRSLVKN DGRDINISGTGLSAIGMGATDMISQS 358
ADGRGIKITG IGVG+GIL T ENYGRSLVKN DGRDIN+SGTGLSAIGMGA DMISQ+

Sbjct: 301 ADGRGIKITGDIGVSGILSTQKENYGRSLVKN DGRDINVSGTGLSAIGMGAADMISQA 360

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
SVSLRESKGQISAANADAMGFN+YNGGGAKQI+ ASSI

Sbjct: 361 SVSLRESKGQISAANADAMGFNSYNGGGAKQILQASSI 398

tr Q99Q27 **Flagellin A (Fragment) [flaA] [Campylobacter jejuni]** 576 AA
align

Score = 696 bits (1796), Expect = 0.0

Identities = 365/400 (91%), Positives = 384/400 (95%), Gaps = 4/400 (1%)

Query: 1 GFRINTNVAALNAKANSDLNSRALDQSLRSLSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTN AALNAKANSDLN+++LD SL+RLSSGLRINSAADDASGMAIADSLRSQANTL

Sbjct: 1 GFRINTNGAALNAKANSDLNAKSLDSSLARLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME

Sbjct: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQ+KA+IGATQSSKIGVTRFETGSQSF

Sbjct: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTVKATIGATQSSKIGVTRFETGSQSF 180

Query: 181 SSGTVGLTIKNGIEDFKFDSVVISTSVGTGLGALAEIINRNADKTGIRATFDVKS VGA 240
+SG VGLTIKNGIEDFKFD+VVISTSVGTGLGALAEIIN+NADKTG+RAT+DVK+ GA

Sbjct: 181 TSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEIINKNADKTGVRATYDVKTTGA 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLT 300
YAIKAG TSQDFAINGV+IGKVDY DGD NGSLISAINAVKDTTGVQASKDENGKLVLT

Sbjct: 241 YAIKAGTTSQDFAINGVIIGKVDYKGDNNGSLISAINAVKDTTGVQASKDENGKLVLT 300

Query: 301 ADGRGIKITGSIGVGAGIL--HTENYGRSLVKN DGRDINISGTGLSAIGMGATDMISQS 358
ADGRGIKITG IGVG+GIL ENYGRSLVKN DGRDIN+SGTGLSAIGMGA DMISQ+

Sbjct: 301 ADGRGIKITGDIGVSGILSAQKENYGRSLVKN DGRDINVSGTGLSAIGMGAADMISQA 360

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQI--IFASSI 396
SVSLRESKGQISAANADAMGFN+YNGGGAKQI + ASSI

Sbjct: 361 SVSLRESKGQISAANADAMGFNSYNGGGAKQILQVQASSI 400

tr Q93NL6 **Flagellin A (Fragment) [flaA] [Campylobacter jejuni]** 557 AA
align

Score = 687 bits (1774), Expect = 0.0

Identities = 358/389 (92%), Positives = 377/389 (96%), Gaps = 2/389 (0%)

```

Query: 10  ALNAKANSDLNSRALDQSLSRSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND 69
          ALNAKANSDLN+++LD SL+RLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND
Sbjct: 1   ALNAKANSDLNAKSLDSSLARLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND 60

Query: 70  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLMEELDNIANTT 129
          ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LMEELDNIANTT
Sbjct: 61  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANTT 120

Query: 130  SFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSFSSGTVGLTI 189
          SFNGKQLLSGGFTNQEFQIGSSSNQ+KA+IGATQSSKIGVTRFETGSQSF+SG VGLTI
Sbjct: 121 SFNGKQLLSGGFTNQEFQIGSSSNQTVKATIGATQSSKIGVTRFETGSQSFTSGVVGLTI 180

Query: 190  KNYNGIEDFKFDSVVISTSVGTGLGALAEIEINRNADKTGIRATFDVKSVMGAYAIKAGNTS 249
          KNYNGIEDFKFD+VVISTSVGTGLGALAEIEIN+NADKTG+RAT+DVK+ GAYAIKAG TS
Sbjct: 181 KNYNGIEDFKFDNVVISTSVGTGLGALAEIEINKNADKTGVRATYDVKTTGAYAIKAGTTS 240

Query: 250  QDFAINGVVIGKVDYSDGDENGLISAINAVKDDTTGVQASKDENGKLVLTSAADGRGIKIT 309
          QDFAINGV+IGKVDY DGD NGSLISAINAVKDDTTGVQASKDENGKLVLTSAADGRGIKIT
Sbjct: 241 QDFAINGVIIGKVDYKDGDNNGSLISAINAVKDDTTGVQASKDENGKLVLTSAADGRGIKIT 300

Query: 310  GSIGVGAGILHT--ENYGRSLSVKNDGRDINISGTGLSAIGMGATDMISQSSVSLRESKG 367
          G IGVG+GIL T ENYGRSLSVKNDGRDIN+SGTGLSAIGMGA DMISQ+SVSLRESKG
Sbjct: 301 GDIGVGSGILSTQKENYGRSLSVKNDGRDINVSGTGLSAIGMGAADMISQASVSLRESKG 360

Query: 368  QISAANADAMGFNAYNGGGAKQIIFASSI 396
          QISAANADAMGFN+YNGGGAKQI+ ASSI
Sbjct: 361 QISAANADAMGFNSYNGGGAKQILQASSI 389

```

tr Q93NL9 **Flagellin A (Fragment) [flaA] [Campylobacter jejuni]** 557 AA
align

Score = 687 bits (1773), Expect = 0.0

Identities = 358/389 (92%), Positives = 377/389 (96%), Gaps = 2/389 (0%)

```

Query: 10  ALNAKANSDLNSRALDQSLSRSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND 69
          ALNAKANSDLN+++LD SL+RLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND
Sbjct: 1   ALNAKANSDLNAKSLDSSLARLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND 60

Query: 70  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLMEELDNIANTT 129
          ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LMEELDNIANTT
Sbjct: 61  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANTT 120

Query: 130  SFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSFSSGTVGLTI 189
          SFNGKQLLSGGFTNQEFQIGSSSNQ+KA+IGATQSSKIGVTRFETGSQSF+SG VGLTI
Sbjct: 121 SFNGKQLLSGGFTNQEFQIGSSSNQTVKATIGATQSSKIGVTRFETGSQSFTSGIVGLTI 180

Query: 190  KNYNGIEDFKFDSVVISTSVGTGLGALAEIEINRNADKTGIRATFDVKSVMGAYAIKAGNTS 249
          KNYNGIEDFKFD+VVISTSVGTGLGALAEIEIN+NADKTG+RAT+DVK+ GAYAIKAG TS
Sbjct: 181 KNYNGIEDFKFDNVVISTSVGTGLGALAEIEINKNADKTGVRATYDVKTTGAYAIKAGTTS 240

Query: 250  QDFAINGVVIGKVDYSDGDENGLISAINAVKDDTTGVQASKDENGKLVLTSAADGRGIKIT 309
          QDFAINGV+IGKVDY DGD NGSLISAINAVKDDTTGVQASKDENGKLVLTSAADGRGIKIT
Sbjct: 241 QDFAINGVIIGKVDYKDGDNNGSLISAINAVKDDTTGVQASKDENGKLVLTSAADGRGIKIT 300

```

Query: 310 GSIGVGAGILHT--ENYGRSLSLVKNDGRDINISGTGLSAIGMGATDMISQSSVSLRESKG 367
 G IGVG+GIL T ENYGRSLSLVKNDGRDIN+SGTGLSAIGMGA DMISQ+SVSLRESKG
 Sbjct: 301 GDIGVGSGILFTQKENYGRSLSLVKNDGRDINVSGTGLSAIGMGAADMISQASVSLRESKG 360

Query: 368 QISAANADAMGFNAYNGGGAKQIIFASSI 396
 QISAANADAMGFN+YNGGGAKQI+ ASSI
 Sbjct: 361 QISAANADAMGFNSYNGGGAKQILQASSI 389

sp P22251 **Flagellin A [flaA] [Campylobacter jejuni]** 575 AA
 FLA2_CAMJE align

Score = 674 bits (1738), Expect = 0.0
 Identities = 351/398 (88%), Positives = 374/398 (93%), Gaps = 4/398 (1%)

Query: 1 GFRINTNVAALNAKANSDLNSRALDQSLRSLSSGLRINSAADDASGMAIADSLRSQANTL 60
 GFRINTNVAALNAKANSDLN+++LD SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
 Sbjct: 1 GFRINTNVAALNAKANSDLNAKSLDASLRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
 Sbjct: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
 ELDNIANTTSFNGKQLLSG FTNQEFQIG+SSNQT+KA+IGATQSSKIGVTRFETG+QSF
 Sbjct: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180

Query: 181 SSGTVGLTIKKNYNGIEDFKFDSVVISTSVGTGLGALAEIINRNADKTGIRATFDVKS VGA 240
 +SG VGLTIKKNYNGIEDFKFD+VVISTSVGTGLGALAEIIN++ADKTG+RAT+DVK+ G
 Sbjct: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKT'TGV 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS 300
 YAIK G TSQDFAINGV IKG++Y DGD NGSLISAINAVKDTTGVQASKDENGKLV LTS
 Sbjct: 241 YAIKEGTTSQDFAINGVTIGKIEYKGDGNGSLISAINAVKDTTGVQASKDENGKLV LTS 300

Query: 301 ADGRGIKITGSIGVGAGIL--HTENYGRSLSLVKNDGRDINISGTGLSAIGMGATDMISQS 358
 ADGRGIKITG IGVG+GIL ENYGRSLSLVKNDGRDINISGT LSAIGMG TDMISQS
 Sbjct: 301 ADGRGIKITGDIGVGSGILANQKENYGRSLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
 SVSLRESKGQISA NADAMGFN+Y GGG + +F ++
 Sbjct: 361 SVSLRESKGQISATNADAMGFNSYKGGG--KFVFTQNV 396

tr Q8G9F3 **Flagellin (Fragment) [flaA] [Campylobacter coli]** 575 AA
 align

Score = 674 bits (1738), Expect = 0.0
 Identities = 352/398 (88%), Positives = 377/398 (94%), Gaps = 4/398 (1%)

Query: 1 GFRINTNVAALNAKANSDLNSRALDQSLRSLSSGLRINSAADDASGMAIADSLRSQANTL 60
 GFRINTN AALNAKANSDLNS++LDQSL+RLSSGLRINSAADDASGMAIADSLRSQA+TL
 Sbjct: 1 GFRINTNGAALNAKANSDLNSKSLDQSLARLSSGLRINSAADDASGMAIADSLRSQASTL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

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      GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME
Sbjct: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121  ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
      ELDNIANTTSFNGKQLLSGGFTNQEFQIG+SSNQTIKA+IGATQSSKIGVTRFETG+QSF
Sbjct: 121  ELDNIANTTSFNGKQLLSGGFTNQEFQIGASSNQTIKATIGATQSSKIGVTRFETGAQSF 180

Query: 181  SSGTVGLTIKNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDVKS VGA 240
      +SG VGLTIKNGIEDFKFD+VVISTSVGTGLGALAEIN++ADKTG+RAT+DVK+ G
Sbjct: 181  TSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKT TGV 240

Query: 241  YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS 300
      YAIK G TSQDFAINGV IGK++Y DGD +GSLISAINAVKDTTGVQASKDENGKLV LTS
Sbjct: 241  YAIKEGTTSQDFAINGVTIGKIEYKDG DGDGSLISAINAVKDTTGVQASKDENGKLV LTS 300

Query: 301  ADGRGIKITGSIGVGAGIL--HTENYGRSLSVKNDGRDINISGTGLSAIGMGATDMISQS 358
      ADGRGIKITG IGVG+GIL ENYGRSLSVKNDGRDINISGT LSAIGMG TDMISQS
Sbjct: 301  ADGRGIKITGDIGVGSGILANQKENYGRSLSVKNDGRDINISGTNLSAIGMGT TDMISQS 360

Query: 359  SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
      SVSLRESKGQISA NADAMGFN+Y GGG +++ +S++
Sbjct: 361  SVSLRESKGQISATNADAMGFNSYKGGG--KLV LSSAV 396

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tr      O85179          Flagellin A [flaA] [Campylobacter jejuni]      576 AA
                                           align

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Score = 674 bits (1738), Expect = 0.0

Identities = 351/398 (88%), Positives = 374/398 (93%), Gaps = 4/398 (1%)

```

Query: 1    GFRINTNVAALNAKANSDLNSRALDQSLSR LSSGLRINSAADDASGMAIADSLRSQANTL 60
      GFRINTNVAALNAKANSDLN+++LD SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 2    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 61

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
      GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 121

Query: 121  ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
      ELDNIANTTSFNGKQLLSG FTNQEFQIG+SSNQTKA+IGATQSSKIGVTRFETG+QSF
Sbjct: 122  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 181

Query: 181  SSGTVGLTIKNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDVKS VGA 240
      +SG VGLTIKNGIEDFKFD+VVISTSVGTGLGALAEIN++ADKTG+RAT+DVK+ G
Sbjct: 182  TSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKT TGV 241

Query: 241  YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS 300
      YAIK G TSQDFAINGV IGK++Y DGD NGSLISAINAVKDTTGVQASKDENGKLV LTS
Sbjct: 242  YAIKEGTTSQDFAINGVTIGKIEYKDG DGDNGSLISAINAVKDTTGVQASKDENGKLV LTS 301

Query: 301  ADGRGIKITGSIGVGAGIL--HTENYGRSLSVKNDGRDINISGTGLSAIGMGATDMISQS 358
      ADGRGIKITG IGVG+GIL ENYGRSLSVKNDGRDINISGT LSAIGMG TDMISQS
Sbjct: 302  ADGRGIKITGDIGVGSGILANQKENYGRSLSVKNDGRDINISGTNLSAIGMGT TDMISQS 361

Query: 359  SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
      SVSLRESKGQISA NADAMGFN+Y GGG + +F ++

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Sbjct: 362 SVSLRESKGQISATNADAMGFNSYKGGG--KFVFTQNV 397

tr Q9R950 **Flagellin A [flaA] [Campylobacter jejuni]** 576 AA
align

Score = 672 bits (1733), Expect = 0.0
Identities = 350/398 (87%), Positives = 374/398 (93%), Gaps = 4/398 (1%)

Query: 1 GFRINTNVAALNAKANSDLNSRALDQSLRLSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTNVAALNAKANSDLN+++LD SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 2 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 61

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 121

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
ELDNIANTTSFNGKQLLSG FTNQEFQIG+SSNQT+KA+IGATQSSKIGVTRFETG+QSF
Sbjct: 122 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 181

Query: 181 SSGTVGLTIKNGYNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDVKS VGA 240
+SG VGLTIKNGYNGIEDFKFD+VVISTSVGTGLGALAEIN++ADKTG+RAT+DVK+ G
Sbjct: 182 TSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTGV 241

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS 300
YAIK G TSQ+FAINGV IGK++Y DGD NGSLISAINAVKDTTGVQASKDENGKLV LTS
Sbjct: 242 YAIKEGTTSQNFAINGVTIGKIEYKGDGNGSLISAINAVKDTTGVQASKDENGKLV LTS 301

Query: 301 ADGRGIKITGSIGVGAGIL--HTENYGRSLVKN DGRDINISGTGLSAIGMGATDMISQS 358
ADGRGIKITG IGVG+GIL ENYGRSLVKN DGRDINISGT LSAIGMG TDMISQS
Sbjct: 302 ADGRGIKITGDIGVGS GILANQKENYGRSLVKN DGRDINISGTNLSAIGMGTTDMISQS 361

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
SVSLRESKGQISA NADAMGFN+Y GGG + +F ++
Sbjct: 362 SVSLRESKGQISATNADAMGFNSYKGGG--KFVFTQNV 397

tr Q9RF26 **Chimeric flagellin A/B [Campylobacter jejuni]** 576 AA
align

Score = 670 bits (1728), Expect = 0.0
Identities = 349/398 (87%), Positives = 373/398 (93%), Gaps = 4/398 (1%)

Query: 1 GFRINTNVAALNAKANSDLNSRALDQSLRLSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTNVAALNAKANSDLN+++LD SLSRLSSGLRINSAADDASGMAIADSLRSQA TL
Sbjct: 2 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQAATL 61

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
GQAI+NGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME
Sbjct: 62 GQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
ELDNIANTTSFNGKQLLSG FTNQEFQIG+SSNQT+KA+IGATQSSKIGVTRFETG+QSF
Sbjct: 122 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 181

Query: 181 SSGTVGLTIKNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDVKS VGA 240
+SG VGLTIKNGIEDFKFD+VVISTSVGTGLGALAEIN++ADKTG+RAT+DVK+ G
Sbjct: 182 TSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGV 241

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDDTTGVQASKDENGKLV LTS 300
YAIK G TSQDFAINGV IGK++Y DGD NGSLISAINAVKDDTTGVQASKDENGKLV LTS
Sbjct: 242 YAIKEGTTSQDFAINGVTIGKIEYKDG DNGSLISAINAVKDDTTGVQASKDENGKLV LTS 301

Query: 301 ADGRGIKITGSIGVGAGIL--HTENYGRSLVKN DGRDINISGTGLSAIGMGATDMISQS 358
ADGRGIKITG IGVG+GIL ENYGRSLVKN DGRDINISGT LSAIGMG TDMISQS
Sbjct: 302 ADGRGIKITGDIGVGS GILANQKENYGRSLVKN DGRDINISGTNLSAIGMGTTDMISQS 361

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
SVSLRESKGQISA NADAMGFN+Y GGG + +F ++
Sbjct: 362 SVSLRESKGQISATNADAMGFNSYKGGG--KFVFTQNV 397

tr Q9R953 **Flagellin A [flaA] [Campylobacter jejuni]** 576 AA
align

Score = 669 bits (1727), Expect = 0.0
Identities = 349/398 (87%), Positives = 373/398 (93%), Gaps = 4/398 (1%)

Query: 1 GFRINTNVAALNAKANS DLNSRALDQSL SRLSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTN AALNAKANS DLN+++LD SL SRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 2 GFRINTNGAALNAKANS DLNAKSLDASL SRLSSGLRINSAADDASGMAIADSLRSQANTL 61

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 121

Query: 121 ELDNIA NTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQS F 180
ELD NIA NTTSFNGKQLLSG FTNQEFQIG+SSNQT+KA+IGATQSSKIGVTRFETG+QS F
Sbjct: 122 ELDNIA NTTSFNGKQLLSGNFTNQEFQIGASSNQT VKATIGATQSSKIGVTRFETGAQS F 181

Query: 181 SSGTVGLTIKNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDVKS VGA 240
+SG VGLTIKNGIEDFKFD+VVISTSVGTGLGALAEIN++ADKTG+RAT+DVK+ G
Sbjct: 182 TSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGV 241

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDDTTGVQASKDENGKLV LTS 300
YAIK G TSQ+FAINGV IGK++Y DGD NGSLISAINAVKDDTTGVQASKDENGKLV LTS
Sbjct: 242 YAIKEGTTSQEFAINGVTIGKIEYKDG DNGSLISAINAVKDDTTGVQASKDENGKLV LTS 301

Query: 301 ADGRGIKITGSIGVGAGIL--HTENYGRSLVKN DGRDINISGTGLSAIGMGATDMISQS 358
ADGRGIKITG IGVG+GIL ENYGRSLVKN DGRDINISGT LSAIGMG TDMISQS
Sbjct: 302 ADGRGIKITGDIGVGS GILANQKENYGRSLVKN DGRDINISGTNLSAIGMGTTDMISQS 361

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
SVSLRESKGQISA NADAMGFN+Y GGG + +F ++
Sbjct: 362 SVSLRESKGQISATNADAMGFNSYKGGG--KFVFTQNV 397

tr O85183 **Flagellin A [flaA] [Campylobacter jejuni]** 576 AA
align

sp P22252 **Flagellin B [flaB] [Campylobacter jejuni]** 575 AA
FLB2_CAMJE align

Score = 660 bits (1703), Expect = 0.0
Identities = 344/398 (86%), Positives = 369/398 (92%), Gaps = 4/398 (1%)

Query: 1 GFRINTNVAALNAKANSDLNSRALDQSLSRSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTN+ ALNA ANS +NS LD+SLSRLSSGLRINSAADDASGMAIADSLRSQA TL
Sbjct: 1 GFRINTNIGALNAHANSVVNSNELDKSLSRSSGLRINSAADDASGMAIADSLRSQAATL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
GQAI+NGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME
Sbjct: 61 GQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
ELDNIANTTSFNGKQLLSG FTNQEFQIG+SSNQTIKA+IGATQSSKIGVTRFETG+QSF
Sbjct: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTIKATIGATQSSKIGVTRFETGAQSF 180

Query: 181 SSGTVGLTIKNGYNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDVKS VGA 240
+SG VGLTIKNGYNGIEDFKFD+VVISTSVGTGLGALAEIN++ADKTG+RAT+DVK+ G
Sbjct: 181 TSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKT TGV 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS 300
YAIK G TSQDFAINGVVIG+++Y DGD NG L+SAINAVKDTTGVQASKDENGKLV LTS
Sbjct: 241 YAIKEGTTSQDFAINGVVIGQINYKGDGDNNGQLVSAINAVKDTTGVQASKDENGKLV LTS 300

Query: 301 ADGRGIKITGSIGVGAGIL--HTENYGRSLVKN DGRDINISGTGLSAIGMGATDMISQS 358
ADGRGIKITG IGVG+GIL ENYGRSLVKN DGRDINISGT LSAIGMG TDMISQS
Sbjct: 301 ADGRGIKITGDIGVGSGILANQKENYGRSLVKN DGRDINISGTNLSAIGMGTTDMISQS 360

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
SVSLRESKGQISA NADAMGFN+Y GGG + +F ++
Sbjct: 361 SVSLRESKGQISATNADAMGFNSYKGGG--KFVFTQNV 396

tr Q9RF25 **Flagellin B [flaB] [Campylobacter jejuni]** 576 AA
align

Score = 660 bits (1703), Expect = 0.0
Identities = 344/398 (86%), Positives = 369/398 (92%), Gaps = 4/398 (1%)

Query: 1 GFRINTNVAALNAKANSDLNSRALDQSLSRSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTN+ ALNA ANS +NS LD+SLSRLSSGLRINSAADDASGMAIADSLRSQA TL
Sbjct: 2 GFRINTNIGALNAHANSVVNSNELDKSLSRSSGLRINSAADDASGMAIADSLRSQAATL 61

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
GQAI+NGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME
Sbjct: 62 GQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
ELDNIANTTSFNGKQLLSG FTNQEFQIG+SSNQTIKA+IGATQSSKIGVTRFETG+QSF
Sbjct: 122 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTIKATIGATQSSKIGVTRFETGAQSF 181

Query: 181 SSGTVGLTIKNGYNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDVKS VGA 240
+SG VGLTIKNGYNGIEDFKFD+VVISTSVGTGLGALAEIN++ADKTG+RAT+DVK+ G

Sbjct: 182 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTTGV 241

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGLISAINAVKDTTGVQASKDENGKLVLT 300
YAIK G TSQDFAINGVVIG+++Y DGD NG L+SAINAVKDTTGVQASKDENGKLVLT

Sbjct: 242 YAIKEGTTSQDFAINGVVIGQINYKGDGDNNGQLVSAINAVKDTTGVQASKDENGKLVLT 301

Query: 301 ADGRGIKITGSIGVGAGIL--HTENYGRSLVKN DGRDINISGTGLSAIGMGATDMISQS 358
ADGRGIKITG IGVG+GIL ENYGRSLVKN DGRDINISGT LSAIGMG TDMISQS

Sbjct: 302 ADGRGIKITGDIGVSGILANQKENYGRSLVKN DGRDINISGTNL SAIGMGTTDMISQS 361

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
SVSLRESKGQISA NADAMGFN+Y GGG + +F ++

Sbjct: 362 SVSLRESKGQISATNADAMGFNSYKGGG--KFVFTQNV 397

tr Q7X516 **FlaB [flaB] [Campylobacter jejuni]** 576 AA
align

Score = 657 bits (1695), Expect = 0.0
Identities = 341/398 (85%), Positives = 368/398 (91%), Gaps = 4/398 (1%)

Query: 1 GFRINTNVAALNAKANSDLNSRALDQSLRSLSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTN+ ALNA ANS +NS LD+SLSRLSSGLRINSAADDASGMAIADSLRSQA TL

Sbjct: 2 GFRINTNIGALNAHANSVVNSNELDKSLRSLSSGLRINSAADDASGMAIADSLRSQAATL 61

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
GQAI+NGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME

Sbjct: 62 GQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 121

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
ELDNIANTTSFNGKQLLSG FTNQEFQIG+SSNQT+KA+IGATQSSKIGVTRFETG+QSF

Sbjct: 122 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 181

Query: 181 SSGTVGLTIKKNYNGIEDFKFDSVVISTSVGTGLGALAEIINRNADKTGIRATFDVKS VGA 240
+SG VGLTIKKNYNGIEDFKFD+VVISTSVGTGLGALAEIIN++ADKTG+RAT+DVK+ G

Sbjct: 182 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTTGV 241

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGLISAINAVKDTTGVQASKDENGKLVLT 300
YAIK G TSQDFAINGV IG+++Y DGD NG L+SAINAVKDTTGVQASKDENGKLVLT

Sbjct: 242 YAIKEGTTSQDFAINGVAIGQINYKGDGDNNGQLVSAINAVKDTTGVQASKDENGKLVLT 301

Query: 301 ADGRGIKITGSIGVGAGIL--HTENYGRSLVKN DGRDINISGTGLSAIGMGATDMISQS 358
ADGRGIKITG IGVG+GIL ENYGRSLVKN DGRDINISGT LSAIGMG TDMISQS

Sbjct: 302 ADGRGIKITGDIGVSGILANQKENYGRSLVKN DGRDINISGTNL SAIGMGTTDMISQS 361

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
SVSLRESKGQISA NADAMGFN+Y GGG + +F ++

Sbjct: 362 SVSLRESKGQISATNADAMGFNSYKGGG--KFVFTQNV 397

tr Q6L5K6 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 568 AA
align

Score = 608 bits (1568), Expect = e-173
Identities = 321/396 (81%), Positives = 351/396 (88%), Gaps = 2/396 (0%)

```

Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLRSLSSGLRINSAADDASGMAIADSLRSQANTL 60
          GFRINTNVA+LNA+AN++LNSRALD SLSRLSSGLRINSAADDASGMAIADSLRSQA+TL
Sbjct: 1   GFRINTNVASLNAQANANLNSRALDTLSRLSSGLRINSAADDASGMAIADSLRSQASTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
          GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADINRLME
Sbjct: 61  GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
          ELDNIANTTSFNGKQLLSGGFTNQEFQIGS SNQ+IKA+IGATQSSKIGVTRFETGS S
Sbjct: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSQSNQSIKATIGATQSSKIGVTRFETGSMNS 180

Query: 181 SSGTVGLTIKKNYNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDVKS VGA 240
          +SG LTIKKNYNGI+DFKF VVISTSVGTG+GALAEINR +D TG+RA F V++ G
Sbjct: 181 TSGIAQLTIKKNYNGIDDFKFQPVVISTSVGTGMGALAEINRVSDVTGVRANFLVETTG 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS 300
          AIKA TSQDF+INGV IG+V+Y DGDENG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241 GAIKADKTSQDFSINGVRIGEVEYKGDENGALISAINSVKDTTGVASKDANGRLVLNS 300

Query: 301 ADGRGIKITGSIGVGAGILHT--ENYGRSLSVKNDGRDINISGTGLSAIGMGATDMISQS 358
          DGRGIKI GS+G+GAG+L ENYGRSLSVKNDG+DI ISGT LS IGMGA DMISQ+
Sbjct: 301 RDGRGIKIEGSMGMGAGVLKADYENYGRSLSVKNDGKDIAISGTNLSTIGMGAADMISQA 360

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFAS 394
          S+SLRESKG I ADAMGFNAY GGG + F+S
Sbjct: 361 SISLRESKGNIDTNVADAMGFNAYKGGGKMIVTFSS 396

```

tr Q6L5K7 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 563 AA
align

Score = 606 bits (1563), Expect = e-172

Identities = 319/396 (80%), Positives = 352/396 (88%), Gaps = 2/396 (0%)

```

Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLRSLSSGLRINSAADDASGMAIADSLRSQANTL 60
          GFRINTNVA+LNA+ N++LNSRALD SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1   GFRINTNVASLNAQNNANLNSRALDTLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
          GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADINRLME
Sbjct: 61  GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
          ELDNIANTTSFNGKQLLSGGFTNQ FQIG+ SNQTI+ASIGATQSSKIGVTRFETGS S
Sbjct: 121 ELDNIANTTSFNGKQLLSGGFTNQSFQIGAQSNTIQASIGATQSSKIGVTRFETGSMNS 180

Query: 181 SSGTVGLTIKKNYNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDVKS VGA 240
          SSG LTIKKNYNGI+DFKF VVIS+SVGTG+GALAEINR AD TG+RA F V++ GA
Sbjct: 181 SSGVAQLTIKKNYNGIDDFKFQPVVISSSVGTGIGALAEINRVADITGVRANFLVQTGA 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS 300
          +IKA TSQDF+INGV +G+V+Y DGDENG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241 GSIKADKTSQDFSINGVKVGEVEYKGDENGALISAINSVKDTTGVASKDANGRLVLNS 300

```

Query: 301 ADGRGIKITGSIGVGAGILHTE--NYGRSLVKN DGRDINISGTGLSAIGMGATDMISQS 358
DGRGI+ITGSIG G+GI+ + N+GRSLVKN DG+DI ISG+GLSAIGMGA DMISQ+
Sbjct: 301 RDGRGIEITGSIGFGSGIMKDDYKNFGRSLVKN DGKDILISGSLSAIGMGAADMISQA 360

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFAS 394
S+SLRESKG I ADAMGFNAY GGG + FA+
Sbjct: 361 SISLRESKGNIDTNVADAMGFNAYKGGGKMIVTFAN 396

tr Q6L5K1 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 568 AA
align

Score = 606 bits (1562), Expect = e-172
Identities = 320/396 (80%), Positives = 350/396 (87%), Gaps = 2/396 (0%)

Query: 1 GFRINTNVAALNAKANS DLNSRALDQSLRLSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTNVA+LNA+AN++LNSRALD SLRLSSGLRINSAADDASGMAIADSLRSQA+TL
Sbjct: 1 GFRINTNVASLNAQANANLNSRALD TSLRLSSGLRINSAADDASGMAIADSLRSQASTL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADINRLME
Sbjct: 61 GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNIANTTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
ELDNIANTT+FNGKQLLSGGFTNQEFQIGS SNQ+IKA+IGATQSSKIGVTRFETGS S
Sbjct: 121 ELDNIANTTAFNGKQLLSGGFTNQEFQIGSQSNQSIKATIGATQSSKIGVTRFETGSM SK 180

Query: 181 SSGTVGLTIKKNYNGIEDFKFDSVVISTSVGTGLGALAE EINRNADKTGIRATFDVKS VGA 240
SG LTIKKNYNGI+DFKF VVISTSVGTG+GALAE EINR AD TG+RA F V++ G
Sbjct: 181 DSGIAQLTIKKNYNGIDDFKFQPVVISTSVGTGMGALAE EINRVADVTGVRANFLVETTGV 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS 300
AIKA TSQDF+INGV IG+V+Y DGDENG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241 GAIKADKTSQDFSINGVRIGEVEYKDG DENGALISAINSVKDTTGV EASKDANGRLVLNS 300

Query: 301 ADGRGIKITGSIGVGAGILHT--ENYGRSLVKN DGRDINISGTGLSAIGMGATDMISQS 358
DGRGIKI GS+G+GAG+L ENYGRSLVKN DG+DI ISG+ LS IGMGAT MISQ+
Sbjct: 301 RDGRGIKIEGSMGMGAGVLKADYENYGRSLVKN DGKDIAISGSLSTIGMGATQMISQA 360

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFAS 394
S+SLRESKG I ADAMGFNAY GGG + F+S
Sbjct: 361 SISLRESKGNIDTNVADAMGFNAYKGGGKMIVTFSS 396

tr Q6L5J8 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 568 AA
align

Score = 604 bits (1558), Expect = e-172
Identities = 319/396 (80%), Positives = 350/396 (87%), Gaps = 2/396 (0%)

Query: 1 GFRINTNVAALNAKANS DLNSRALDQSLRLSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTNVA+LNA+AN++LNSRALD SLRLSSGLRINSAADDASGMAIADSLRSQA+TL
Sbjct: 1 GFRINTNVASLNAQANANLNSRALD TSLRLSSGLRINSAADDASGMAIADSLRSQASTL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

```

      GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADINRLME
Sbjct: 61 GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNIANTTTFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
      ELDNIANTT+FNGKQLLSGGFTNQEFQIG+ SNQ+IKA+IGATQSSKIGVTRFETGS S
Sbjct: 121 ELDNIANTTAFNGKQLLSGGFTNQEFQIGAQSNQSIKATIGATQSSKIGVTRFETGSMSN 180

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDVKSVA 240
      +SG LTIKNYNGI+DFKF VVISTSVGTG+GALAEINR AD TG+RA F V++ G
Sbjct: 181 TSGIAQLTIKNYNGIDDFKFQPVVISTSVGTGMGALAEINRVADVTGVRANFLVETTV 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLS 300
      AIKA TSQDF INGV IG+V+Y DGDENG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241 GAIKADKTSQDFTINGVRIGEVEYKGDENGALISAINSVKDTTGVASKDANGRLVLNS 300

Query: 301 ADGRGIKITGSIGVGAGILHT--ENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQS 358
      DGRGIKI GS+G+GAG+L ENYGRLSLVKNDG+DI ISG+ LS IGMGA DMISQ+
Sbjct: 301 RDGRGIKIEGSMGMGAGVLKADYENYGRLSLVKNDGKDIAISGSNLSTIGMGAGDMISQA 360

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFAS 394
      S+SLRESKG I ADAMGFNAY GGG + F+S
Sbjct: 361 SISLRESKGNIDTNVADAMGFNAYKGGGKMIVTFSS 396

```

```

tr   Q6L5K8      Flagellin (Fragment) [flaA] [Campylobacter lari] 567 AA
                                align

```

Score = 604 bits (1557), Expect = e-171

Identities = 319/396 (80%), Positives = 351/396 (88%), Gaps = 2/396 (0%)

```

Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRSLSSGLRINSAADDASGMAIADSLRSQANTL 60
      GFRINTNVA+LNA+ N++LNSRALD SLRSLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1   GFRINTNVAASLNAQNNANLNSRALDSSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
      GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADINRLME
Sbjct: 61  GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNIANTTTFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
      ELDNIANTT+FNGKQLLSGGFTNQ FQIG+ SNQTI+ASIGATQSSKIGVTRFETGS S
Sbjct: 121 ELDNIANTTAFNGKQLLSGGFTNQSFQIGAQSNQTIQASIGATQSSKIGVTRFETGSMSH 180

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDVKSVA 240
      SSG LTIKNYNGI+DFKF VVIS+SVGTG+GALAEINR AD TG+RA F V++ GA
Sbjct: 181 SSGVAQLTIKNYNGIDDFKFQPVVISSSVGTGMGALAEINRVADVTGVRANFLVQTTGA 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLS 300
      +IKA TSQDF INGV IG+V+Y DGDENG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241 GSIKADKTSQDFTINGVKIGEVEYKGDENGALISAINSVKDTTGVASKDANGRLVLNS 300

Query: 301 ADGRGIKITGSIGVGAGILHTE--NYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQS 358
      DGRGI+ITG++GVG+G+L + N+GRLSLVKNDG+DI ISG+GLS IGMGA DMISQ+
Sbjct: 301 RDGRGIEITGNMGVGSVGLKDDYKNFGRLSLVKNDGKDILISGSGLSFIGMGAGDMISQA 360

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFAS 394
      SVSLRESKG I ADAMGFNAY GGG I F+S

```

Sbjct: 361 SVSLRESKGNIDTHVADAMGFNAYKGGGKMVITFSS 396

tr Q6L5K2 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 567 AA
align

Score = 603 bits (1555), Expect = e-171

Identities = 317/396 (80%), Positives = 351/396 (88%), Gaps = 2/396 (0%)

Query: 1 GFRINTNVAALNAKANSDLNSRALDQSLSRSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTNVA+LNA+ N++LNSRALD SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1 GFRINTNVASLNAQNNANLNSRALDSSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINRLME 120
GQAI+NGNDALGILQTADKAMDEQLKILDITIK KATQAAQDGQS KTR MLQADINRLME
Sbjct: 61 GQAINNGNDALGILQTADKAMDEQLKILDITIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
ELDNIANTT+FNGKQLLSGGFTNQ FQIG+ SNQTI+ASIGATQSSKIGVTRFETGS S
Sbjct: 121 ELDNIANTTAFNGKQLLSGGFTNQSFQIGAQSNTIQASIGATQSSKIGVTRFETGSMH 180

Query: 181 SSGTVGLTIKKNYNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDVKS VGA 240
SSG LTIKKNYNGI+DFKF VVIS+SVGTG+GALAEINR AD TG+RA F V++ GA
Sbjct: 181 SSGVAQLTIKKNYNGIDDFKFQPVVISSSVGTGMGALAEINRVADVTGVRANFLVQTTGA 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS 300
+IKA TSQDF INGV IG+V+Y DGDENG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241 GSIKADKTSQDFTINGVKIGEVEYKDGDENGALISAINSVKDTTGV EASKDANGRLVLNS 300

Query: 301 ADGRGIKITGSIGVGAGILHTE--NYGRSLSVKNDGRDINISGTGLSAIGMGATDMISQS 358
DGRGI+ITG++GVC+G+L + N+GRSLSVKNDG+DI ISG+GLS IGMGA DMISQ+
Sbjct: 301 RDGRGIEITGNMGVGSGLVLDYKFNFRSLSVKNDGKDILISGSLSFIMGAGDMISQA 360

Query: 359 SVSLRESKQGISANADAMGFNAYNGGGAKQIIFAS 394
S+SLRESKG I ADAMGFNAY GGG + F+S
Sbjct: 361 SISLRESKGNIDTHIADAMGFNAYKGGGKMVITFSS 396

tr Q6L5K9 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 567 AA
align

Score = 602 bits (1553), Expect = e-171

Identities = 318/396 (80%), Positives = 350/396 (88%), Gaps = 2/396 (0%)

Query: 1 GFRINTNVAALNAKANSDLNSRALDQSLSRSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTNVA+LNA+ N++LNSRALD SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1 GFRINTNVASLNAQNNANLNSRALDSSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINRLME 120
GQAI+NGNDALGILQTADKAMDEQLKILDITIK KATQAAQDGQS KTR MLQADINRLME
Sbjct: 61 GQAINNGNDALGILQTADKAMDEQLKILDITIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
ELDNIANTT+FNGKQLLSGGFTNQ FQIG+ SNQTI+A IGATQSSKIGVTRFETGS S
Sbjct: 121 ELDNIANTTAFNGKQLLSGGFTNQSFQIGAQSNTIQAGIGATQSSKIGVTRFETGSMH 180

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Search for

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If your question is not covered, please contact [<helpdesk@expasy.org>](mailto:helpdesk@expasy.org).

NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

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Query length: 420 AA (of which 5% low-complexity regions filtered out)
Date run: 2004-09-02 16:29:13 UTC+0100 on sib-gml.unil.ch
Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]
Database: EXPASY/UniProt
1,544,870 sequences; 494,584,931 total letters

Taxonomic view	NiceBlast view	Printable view
--------------------------------	--------------------------------	--------------------------------

List of potentially matching sequences

Send selected sequences to

☐ Include query sequence

	Db	AC	Description	Score	E-value
<input type="checkbox"/>	sp	P27053	FLAA_CAMCO Flagellin A [flaA] [Campylobacter coli]	750	0.0
<input type="checkbox"/>	tr	Q84IB9	Flagellin (Fragment) [flaA] [Campylobacter jejuni]	736	0.0
<input type="checkbox"/>	tr	Q46009	Flagellin [Campylobacter coli]	724	0.0
<input type="checkbox"/>	sp	P18245	FLAB_CAMCO Flagellin B (Flagellin N) [flaB] [Campyloba...]	723	0.0
<input type="checkbox"/>	tr	Q9RPY6	Flagellin A [flaA] [Campylobacter jejuni]	722	0.0
<input type="checkbox"/>	tr	Q99QL6	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	702	0.0
<input type="checkbox"/>	tr	Q99Q27	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	696	0.0
<input type="checkbox"/>	tr	Q93NL6	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	687	0.0
<input type="checkbox"/>	tr	Q93NL9	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	687	0.0
<input type="checkbox"/>	sp	P22251	FLA2_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	674	0.0

<input type="checkbox"/>	tr	Q8G9F3	Flagellin (Fragment) [flaA] [Campylobacter coli]	674	0.0
<input type="checkbox"/>	tr	Q85179	Flagellin A [flaA] [Campylobacter jejuni]	674	0.0
<input type="checkbox"/>	tr	Q9R950	Flagellin A [flaA] [Campylobacter jejuni]	672	0.0
<input type="checkbox"/>	tr	Q9RF26	Chimeric flagellin A/B [Campylobacter jejuni]	670	0.0
<input type="checkbox"/>	tr	Q9R953	Flagellin A [flaA] [Campylobacter jejuni]	669	0.0
<input type="checkbox"/>	tr	Q85183	Flagellin A [flaA] [Campylobacter jejuni]	667	0.0
<input type="checkbox"/>	sp	P22252	FLB2_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	660	0.0
<input type="checkbox"/>	tr	Q9RF25	Flagellin B [flaB] [Campylobacter jejuni]	660	0.0
<input type="checkbox"/>	tr	Q7X516	FlaB [flaB] [Campylobacter jejuni]	657	0.0
<input type="checkbox"/>	tr	Q6L5K6	Flagellin (Fragment) [flaA] [Campylobacter lari]	608	e-173
<input type="checkbox"/>	tr	Q6L5K7	Flagellin (Fragment) [flaA] [Campylobacter lari]	606	e-172
<input type="checkbox"/>	tr	Q6L5K1	Flagellin (Fragment) [flaA] [Campylobacter lari]	606	e-172
<input type="checkbox"/>	tr	Q6L5J8	Flagellin (Fragment) [flaA] [Campylobacter lari]	604	e-172
<input type="checkbox"/>	tr	Q6L5K8	Flagellin (Fragment) [flaA] [Campylobacter lari]	604	e-171
<input type="checkbox"/>	tr	Q6L5K2	Flagellin (Fragment) [flaA] [Campylobacter lari]	603	e-171
<input type="checkbox"/>	tr	Q6L5K9	Flagellin (Fragment) [flaA] [Campylobacter lari]	602	e-171
<input type="checkbox"/>	tr	Q6L5J9	Flagellin (Fragment) [flaA] [Campylobacter lari]	602	e-171
<input type="checkbox"/>	tr	Q6L5J6	Flagellin (Fragment) [flaA] [Campylobacter lari]	600	e-170
<input type="checkbox"/>	tr	Q6L5K4	Flagellin (Fragment) [flaA] [Campylobacter lari]	600	e-170
<input type="checkbox"/>	tr	Q6L5K5	Flagellin (Fragment) [flaA] [Campylobacter lari]	599	e-170
<input type="checkbox"/>	tr	Q6L5J7	Flagellin (Fragment) [flaA] [Campylobacter lari]	599	e-170
<input type="checkbox"/>	tr	Q6L5L1	Flagellin (Fragment) [flaA] [Campylobacter lari]	598	e-170
<input type="checkbox"/>	tr	Q6L5L0	Flagellin (Fragment) [flaA] [Campylobacter lari]	598	e-170
<input type="checkbox"/>	tr	Q6L5K0	Flagellin (Fragment) [flaA] [Campylobacter lari]	598	e-170
<input type="checkbox"/>	sp	Q46113	FLA3_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	597	e-169
<input type="checkbox"/>	tr	Q85180	Flagellin A [flaA] [Campylobacter jejuni]	590	e-167
<input type="checkbox"/>	tr	Q84IB8	Flagellin (Fragment) [flaA] [Campylobacter jejuni]	590	e-167
<input type="checkbox"/>	tr	Q6L5K3	Flagellin (Fragment) [flaA] [Campylobacter lari]	590	e-167
<input type="checkbox"/>	tr	Q9R952	Flagellin A [flaA] [Campylobacter jejuni]	589	e-167
<input type="checkbox"/>	tr	Q30696	Flagellin A [flaA] [Campylobacter jejuni]	588	e-167
<input type="checkbox"/>	tr	Q8G9F1	Flagellin (Fragment) [flaA] [Campylobacter coli]	588	e-167
<input type="checkbox"/>	tr	Q85182	Flagellin A [flaA] [Campylobacter jejuni]	586	e-166
<input type="checkbox"/>	tr	Q9R949	Flagellin A [flaA] [Campylobacter jejuni]	586	e-166
<input type="checkbox"/>	tr	Q34938	Flagellin A [flaA] [Campylobacter jejuni]	585	e-166
<input type="checkbox"/>	sp	P56963	FLA1_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	585	e-166
<input type="checkbox"/>	tr	Q8G9F2	Flagellin (Fragment) [flaA] [Campylobacter jejuni]	584	e-166
<input type="checkbox"/>	tr	Q30689	Flagellin A [flaA] [Campylobacter jejuni]	583	e-165
<input type="checkbox"/>	sp	Q46114	FLB3_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	581	e-165
<input type="checkbox"/>	tr	Q8G9F0	Flagellin (Fragment) [flaA] [Campylobacter jejuni]	578	e-164
<input type="checkbox"/>	tr	Q93NL8	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	572	e-162
<input type="checkbox"/>	tr	Q79AR6	Flagellin [flaA] [Campylobacter jejuni]	572	e-162
<input type="checkbox"/>	tr	Q933V4	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	570	e-161
<input type="checkbox"/>	tr	Q85181	Flagellin B [flaB] [Campylobacter jejuni]	570	e-161
<input type="checkbox"/>	tr	Q93NL7	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	569	e-161
<input type="checkbox"/>	sp	P56964	FLB1_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	566	e-160

<input type="checkbox"/>	tr Q9R954	Flagellin B [flaB] [Campylobacter jejuni]	565	e-160
<input type="checkbox"/>	tr Q9R951	Flagellin B [flaB] [Campylobacter jejuni]	564	e-160
<input type="checkbox"/>	tr P96751	Flagellin (Fragment) [flaA] [Campylobacter sp]	561	e-159
<input type="checkbox"/>	tr P96752	Flagellin [flaB] [Campylobacter sp]	559	e-158
<input type="checkbox"/>	tr Q93GT4	Flagellin (Fragment) [flaA] [Campylobacter lari]	489	e-137
<input type="checkbox"/>	tr Q93R24	Flagellin (Fragment) [flaA] [Campylobacter lari]	488	e-137
<input type="checkbox"/>	tr Q84IC8	Flagellin (Fragment) [flaA] [Campylobacter lari]	483	e-135
<input type="checkbox"/>	tr Q84IC3	Flagellin (Fragment) [flaA] [Campylobacter lari]	482	e-135
<input type="checkbox"/>	tr Q84IC6	Flagellin (Fragment) [flaA] [Campylobacter lari]	481	e-135
<input type="checkbox"/>	tr Q84IC5	Flagellin (Fragment) [flaA] [Campylobacter lari]	481	e-135
<input type="checkbox"/>	tr Q84IC4	Flagellin (Fragment) [flaA] [Campylobacter lari]	481	e-135
<input type="checkbox"/>	tr Q8RTY4	Flagellin (Fragment) [flaA] [Campylobacter lari]	479	e-134
<input type="checkbox"/>	tr Q84IC9	Flagellin (Fragment) [flaA] [Campylobacter lari]	479	e-134
<input type="checkbox"/>	tr Q93GT1	Flagellin (Fragment) [flaA] [Campylobacter lari]	478	e-134
<input type="checkbox"/>	tr Q84IC7	Flagellin (Fragment) [flaA] [Campylobacter lari]	478	e-133
<input type="checkbox"/>	tr Q84IC1	Flagellin (Fragment) [flaA] [Campylobacter lari]	473	e-132
<input type="checkbox"/>	tr Q93GT2	Flagellin (Fragment) [flaA] [Campylobacter lari]	473	e-132
<input type="checkbox"/>	tr Q84IC2	Flagellin (Fragment) [flaA] [Campylobacter lari]	471	e-131
<input type="checkbox"/>	tr Q93GT3	Flagellin (Fragment) [flaA] [Campylobacter lari]	463	e-129
<input type="checkbox"/>	tr Q46462	Flagellin (Fragment) [fla2] [Campylobacter upsaliensis]	453	e-126
<input type="checkbox"/>	tr Q46461	Flagellin (Fragment) [fla1] [Campylobacter upsaliensis]	444	e-123
<input type="checkbox"/>	tr Q84IC0	Flagellin (Fragment) [flaA] [Campylobacter lari]	424	e-117
<input type="checkbox"/>	tr Q7M7N1	FLAGELLIN B [FLAB] [Wolinella succinogenes]	383	e-105
<input type="checkbox"/>	tr Q7X2D0	Flagellin B [flaB] [Helicobacter pylori (Campylobacter...]	380	e-104
<input type="checkbox"/>	tr Q56746	Flagellin [flag] [Wolinella succinogenes]	379	e-104
<input type="checkbox"/>	sp Q07911	FLAB_HELPY Flagellin B (Flagellin N) [flaB] [Helicobac...]	376	e-103
<input type="checkbox"/>	sp Q9ZMV8	FLAB_HELPJ Flagellin B (Flagellin N) [flaB] [Helicobac...]	376	e-103
<input type="checkbox"/>	tr Q8RNU8	Flagellin B subunit [flaB] [Helicobacter pylori (Campy...]	376	e-103
<input type="checkbox"/>	tr Q6VYQ1	Flagellin B [flaB] [Helicobacter pylori (Campylobacter...]	376	e-103
<input type="checkbox"/>	tr Q8GD49	Flagellin [flaB] [Helicobacter pylori (Campylobacter p...]	375	e-103
<input type="checkbox"/>	sp Q07910	FLAB_HELMU Flagellin B (Flagellin N) [flaB] [Helicobac...]	368	e-100
<input type="checkbox"/>	tr Q7X2D1	Flagellin A [flaA] [Helicobacter pylori (Campylobacter...]	365	e-100
<input type="checkbox"/>	tr Q9XB37	Flagellin B [flaB] [Helicobacter felis]	365	e-100
<input type="checkbox"/>	tr Q7TTM9	Major flagellin subunit FlaA_1 (Major flagellin subuni...]	363	3e-99
<input type="checkbox"/>	sp Q03843	FLAA_HELPY Flagellin A [flaA] [Helicobacter pylori (Ca...]	361	1e-98
<input type="checkbox"/>	sp Q9XB38	FLAA_HELFE Flagellin A [flaA] [Helicobacter felis]	358	1e-97
<input type="checkbox"/>	tr Q6VYQ2	Flagellin A [flaA] [Helicobacter pylori (Campylobacter...]	358	1e-97
<input type="checkbox"/>	tr Q7VF81	Minor flagellin subunit FlaB [flaB] [Helicobacter hepa...]	356	5e-97
<input type="checkbox"/>	sp P50612	FLAA_HELMU Flagellin A [flaA] [Helicobacter mustelae]	345	9e-94
<input type="checkbox"/>	tr Q8VN93	Flagellin B (Fragment) [flaB] [Helicobacter pylori (Ca...]	335	1e-90
<input type="checkbox"/>	tr Q8VN92	Flagellin B (Fragment) [flaB] [Helicobacter pylori (Ca...]	334	2e-90
<input type="checkbox"/>	tr Q93NM0	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	332	8e-90
<input type="checkbox"/>	tr Q93NM1	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	332	1e-89
<input type="checkbox"/>	tr Q8VN91	Flagellin A (Fragment) [flaA] [Helicobacter pylori (Ca...]	330	2e-89
<input type="checkbox"/>	tr Q8VN90	Flagellin A (Fragment) [flaA] [Helicobacter pylori (Ca...]	330	2e-89

Graphical overview of the alignments

[Click here](#) to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs
([? Help](#)) (use ScanProsite for more details about PROSITE matches)

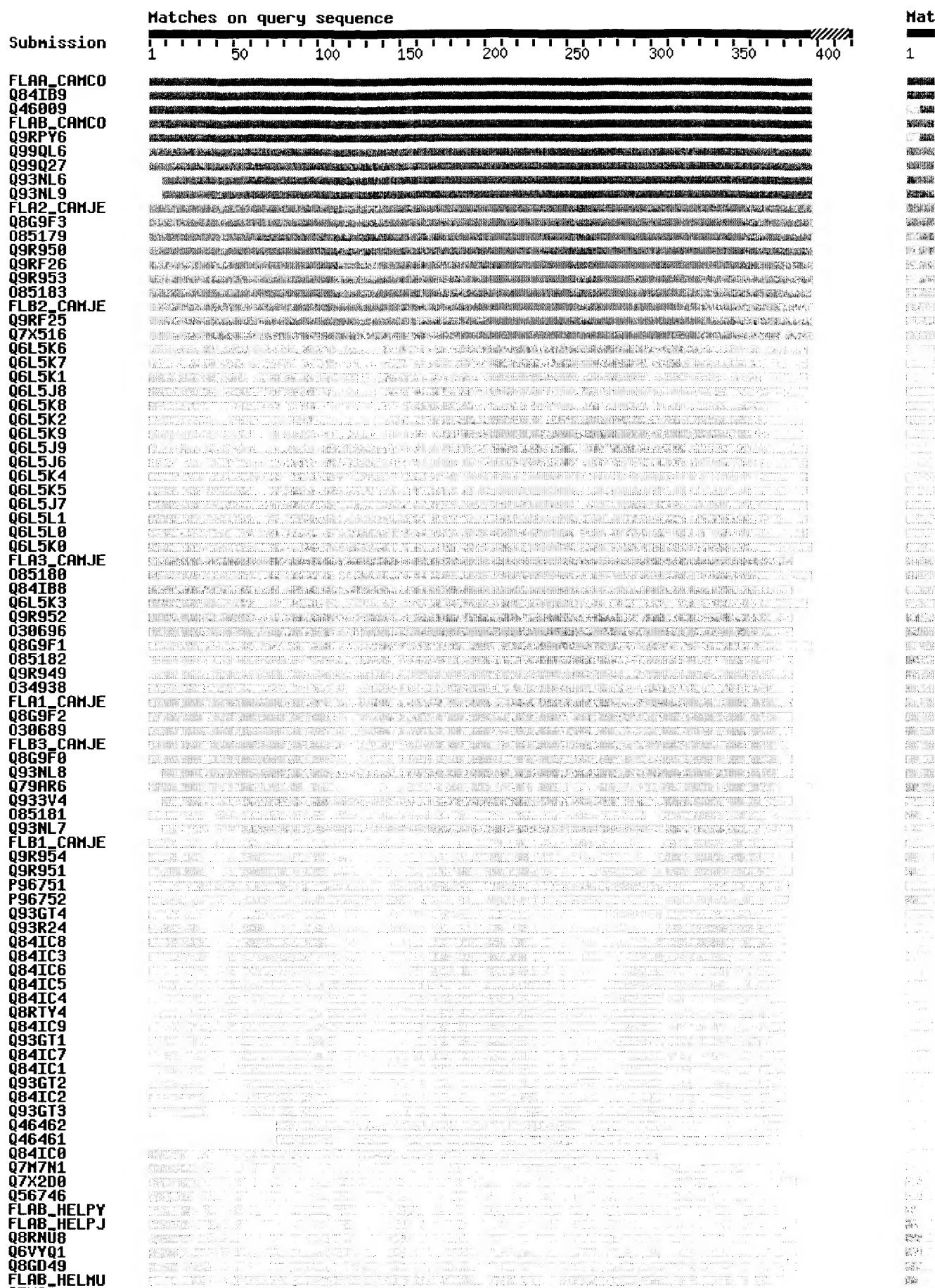
Profile hits

Pfam hits

Flagellin_N

Flagellin_

Flagelli



Alignments

sp P27053 **Flagellin A [flaA] [Campylobacter coli]** 572 AA
FLAA_CAMCO align

Score = 750 bits (1937), Expect = 0.0
Identities = 396/396 (100%), Positives = 396/396 (100%)

Query: 1 GFRINTNVAALNAKANSDLNSRALDQSLSRSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTNVAALNAKANSDLNSRALDQSLSRSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1 GFRINTNVAALNAKANSDLNSRALDQSLSRSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME
Sbjct: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF
Sbjct: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180

Query: 181 SSGTVGLTIKNGYNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDVKS VGA 240
SSGTVGLTIKNGYNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDVKS VGA
Sbjct: 181 SSGTVGLTIKNGYNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDVKS VGA 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS 300
YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS
Sbjct: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS 300

Query: 301 ADGRGIKITGSIGVGAGILHTENYGRSLSVKNDGRDINISGTGLSAIGMGATDMISQSSV 360
ADGRGIKITGSIGVGAGILHTENYGRSLSVKNDGRDINISGTGLSAIGMGATDMISQSSV
Sbjct: 301 ADGRGIKITGSIGVGAGILHTENYGRSLSVKNDGRDINISGTGLSAIGMGATDMISQSSV 360

Query: 361 SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI
Sbjct: 361 SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396

tr Q84IB9 **Flagellin (Fragment) [flaA] [Campylobacter jejuni]** 572 AA
align

Score = 736 bits (1901), Expect = 0.0
Identities = 389/396 (98%), Positives = 392/396 (98%)

Query: 1 GFRINTNVAALNAKANSDLNSRALDQSLSRSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTN AALNAKANSDLNSRALDQSLSRSSGLRINSAADDASGMAIADSLRSQANT+
Sbjct: 1 GFRINTNGAALNAKANSDLNSRALDQSLSRSSGLRINSAADDASGMAIADSLRSQANTM 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
GQAISNG+DALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME
Sbjct: 61 GQAISNGDDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF
Sbjct: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180

Query: 181 SSGTVGLTIKYNNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDVKS VGA 240
SSGTVGLTIKYNNGIEDFKF +VVISTSVGTGLGALAEINRNADKTGIRATFDVKS VGA
Sbjct: 181 SSGTVGLTIKYNNGIEDFKFQNVVISTSVGTGLGALAEINRNADKTGIRATFDVKS VGA 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS 300
Y IKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS
Sbjct: 241 YTIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS 300

Query: 301 ADGRGIKITGSIGVGAGILHTENYGRSLVKN DGRDINISGTGLSAIGMGATDMISQSSV 360
ADGRGIKITGSIGVGAGILHTENYGRSLVKN GRDINISGTGLSAIGMGATDMISQSSV
Sbjct: 301 ADGRGIKITGSIGVGAGILHTENYGRSLVKNVGRDINISGTGLSAIGMGATDMISQSSV 360

Query: 361 SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI
Sbjct: 361 SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396

tr Q46009 Flagellin [Campylobacter coli] 572 AA
align

Score = 724 bits (1869), Expect = 0.0
Identities = 385/396 (97%), Positives = 389/396 (98%), Gaps = 1/396 (0%)

Query: 1 GFRINTNVAALNAKANS DLNSRALDQSL SRLSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTNVAALNAKANS DLNSRALDQSL SRLSSGLRINSAAD ASGMAIADSLRSQANTL
Sbjct: 2 GFRINTNVAALNAKANS DLNSRALDQSL SRLSSGLRINSAADVASGMAIADSLRSQANTL 61

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAA+DGQSLKTRTMLQADINRLME
Sbjct: 62 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAEDGQSLKTRTMLQADINRLME 121

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQS F 180
ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTR ++ F
Sbjct: 122 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRLNRFTK-F 180

Query: 181 SSGTVGLTIKYNNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDVKS VGA 240
SSGTVGLTIKYNNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFD+KSVGA
Sbjct: 181 SSGTVGLTIKYNNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDLKS VGA 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS 300
YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS
Sbjct: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS 300

Query: 301 ADGRGIKITGSIGVGAGILHTENYGRSLVKN DGRDINISGTGLSAIGMGATDMISQSSV 360
ADGRGIKITGSIGVGAGILHTENYGRSLVKN DGRDINISGTG SAIGMGATDMISQSSV
Sbjct: 301 ADGRGIKITGSIGVGAGILHTENYGRSLVKN DGRDINISGTGFS AIGMGATDMISQSSV 360

Query: 361 SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI
Sbjct: 361 SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396

sp P18245 Flagellin B (Flagellin N) [flaB] [Campylobacter coli] 572 AA
FLAB_CAMCO
align

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tr      Q99QL6      Flagellin A (Fragment) [flaA] [Campylobacter jejuni] 574 AA
                                align

Score = 702 bits (1813), Expect = 0.0
Identities = 366/398 (91%), Positives = 385/398 (95%), Gaps = 2/398 (0%)

Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTN AALNAKANSDLN+++LD SL+RLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1   GFRINTNGAALNAKANSDLNAKSLDSSSLARLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINRLME 120
           GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 61   GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINKLME 120

Query: 121  ELDNIIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIIANTTSFNGKQLLSGGFTNQEFQIGSSSNQT+KA+IGATQSSKIGVTRFETGSQSF
Sbjct: 121  ELDNIIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTVKATIGATQSSKIGVTRFETGSQSF 180

Query: 181  SSGTVGLTIKYNNGIEDFKFDSVVISTSVGTGLGALAEIINRNADKTGIRATFDVKSVA 240
           +SG VGLTIKYNNGIEDFKFD+VVISTSVGTGLGALAEIIN+NADKTG+RAT+DVK+ GA

```

Sbjct: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEIINKNADKTGVRATYDVKTTGA 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLT 300
YAIKAG TSQDFAINGV+IGKVDY DGD NGSLISAINAVKDTTGVQASKDENGKLVLT

Sbjct: 241 YAIKAGTTSQDFAINGVIIGKVDYKGDNNGSLISAINAVKDTTGVQASKDENGKLVLT 300

Query: 301 ADGRGIKITGSIGVGAGILHT--ENYGRSLVKN DGRDINISGTGLSAIGMGATDMISQS 358
ADGRGIKITG IGVG+GIL T ENYGRSLVKN DGRDIN+SGTGLSAIGMGA DMISQ+

Sbjct: 301 ADGRGIKITGDIGVSGILSTQKENYGRSLVKN DGRDINVSGTGLSAIGMGAADMISQA 360

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
SVSLRESKGQISAANADAMGFN+YNGGGAKQI+ ASSI

Sbjct: 361 SVSLRESKGQISAANADAMGFNSYNGGGAKQILQASSI 398

tr Q99Q27 **Flagellin A (Fragment) [flaA] [Campylobacter jejuni]** 576 AA
align

Score = 696 bits (1796), Expect = 0.0

Identities = 365/400 (91%), Positives = 384/400 (95%), Gaps = 4/400 (1%)

Query: 1 GFRINTNVAALNAKANSDLNSRALDQSLRSLSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTN AALNAKANSDLN+++LD SL+RLSSGLRINSAADDASGMAIADSLRSQANTL

Sbjct: 1 GFRINTNGAALNAKANSDLNNAKSLDSSLARLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME

Sbjct: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQ+KA+IGATQSSKIGVTRFETGSQSF

Sbjct: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTVKATIGATQSSKIGVTRFETGSQSF 180

Query: 181 SSGTVGLTIKKNYNGIEDFKFDSVVISTSVGTGLGALAEIINRNADKTGIRATFDVKSVA 240
+SG VGLTIKKNYNGIEDFKFD+VVISTSVGTGLGALAEIIN+NADKTG+RAT+DVK+ GA

Sbjct: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEIINKNADKTGVRATYDVKTTGA 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLT 300
YAIKAG TSQDFAINGV+IGKVDY DGD NGSLISAINAVKDTTGVQASKDENGKLVLT

Sbjct: 241 YAIKAGTTSQDFAINGVIIGKVDYKGDNNGSLISAINAVKDTTGVQASKDENGKLVLT 300

Query: 301 ADGRGIKITGSIGVGAGIL--HTENYGRSLVKN DGRDINISGTGLSAIGMGATDMISQS 358
ADGRGIKITG IGVG+GIL ENYGRSLVKN DGRDIN+SGTGLSAIGMGA DMISQ+

Sbjct: 301 ADGRGIKITGDIGVSGILSAQKENYGRSLVKN DGRDINVSGTGLSAIGMGAADMISQA 360

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQI--IFASSI 396
SVSLRESKGQISAANADAMGFN+YNGGGAKQI + ASSI

Sbjct: 361 SVSLRESKGQISAANADAMGFNSYNGGGAKQILQVQASSI 400

tr Q93NL6 **Flagellin A (Fragment) [flaA] [Campylobacter jejuni]** 557 AA
align

Score = 687 bits (1774), Expect = 0.0

Identities = 358/389 (92%), Positives = 377/389 (96%), Gaps = 2/389 (0%)

```

Query: 10  ALNAKANSDLNSRALDQSLSRLLSSGLRINSAADDASGMAIADSLRSQANTLGQAIISNGND 69
          ALNAKANSDLN+++LD SL+RLSSGLRINSAADDASGMAIADSLRSQANTLGQAIISNGND
Sbjct: 1   ALNAKANSDLNAKSLDSSLARLSSGLRINSAADDASGMAIADSLRSQANTLGQAIISNGND 60

Query: 70  ALGILQTADKAMDEQLKILDITIKTKATQAAQDQGQSLKTRTMLQADINRLMEELDNIANTT 129
          ALGILQTADKAMDEQLKILDITIKTKATQAAQDQGQSLKTRTMLQADIN+LMEELDNIANTT
Sbjct: 61  ALGILQTADKAMDEQLKILDITIKTKATQAAQDQGQSLKTRTMLQADINKLMEELDNIANTT 120

Query: 130 SFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSFSSTVGLTI 189
          SFNGKQLLSGGFTNQEFQIGSSSNQT+KA+IGATQSSKIGVTRFETGSQSFS+SG VGLTI
Sbjct: 121 SFNGKQLLSGGFTNQEFQIGSSSNQTVKATIGATQSSKIGVTRFETGSQSFTSGVVGLTI 180

Query: 190 KNYNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDVKSVGAYAIKAGNTS 249
          KNYNGIEDFKFD+VVISTSVGTGLGALAEIN+NADKTG+RAT+DVK+ GAYAIKAG TS
Sbjct: 181 KNYNGIEDFKFDNVVISTSVGTGLGALAEINKNADKTGVRATYDVKTTGAYAIKAGTTS 240

Query: 250 QDFAINGVVIGKVDYSDGDENGSLISAINAVKDDTTGVQASKDENGKLVLTSAADGRGIKIT 309
          QDFAINGV+IGKVDY DGD NGSLISAINAVKDDTTGVQASKDENGKLVLTSAADGRGIKIT
Sbjct: 241 QDFAINGV+IGKVDYKDGDNNGSLISAINAVKDDTTGVQASKDENGKLVLTSAADGRGIKIT 300

Query: 310 GSIGVGAGILHT--ENYGRSLSLVKNDGRDINISGTGLSAIGMGATDMISQSSVSLRESKG 367
          G IGVG+GIL T ENYGRSLSLVKNDGRDIN+SGTGLSAIGMGA DMISQ+SVSLRESKG
Sbjct: 301 GDIGVGSGILSTQKENYGRSLSLVKNDGRDINVS GTGLSAIGMGADMISQASVSLRESKG 360

Query: 368 QISAANADAMGFNAYNGGGAKQIIFASSI 396
          QISAANADAMGFN+YNGGGAKQI+ ASSI
Sbjct: 361 QISAANADAMGFNSYNGGGAKQILQASSI 389

```

tr Q93NL9 **Flagellin A (Fragment) [flaA] [Campylobacter jejuni]** 557 AA
align

Score = 687 bits (1773), Expect = 0.0

Identities = 358/389 (92%), Positives = 377/389 (96%), Gaps = 2/389 (0%)

```

Query: 10  ALNAKANSDLNSRALDQSLSRLLSSGLRINSAADDASGMAIADSLRSQANTLGQAIISNGND 69
          ALNAKANSDLN+++LD SL+RLSSGLRINSAADDASGMAIADSLRSQANTLGQAIISNGND
Sbjct: 1   ALNAKANSDLNAKSLDSSLARLSSGLRINSAADDASGMAIADSLRSQANTLGQAIISNGND 60

Query: 70  ALGILQTADKAMDEQLKILDITIKTKATQAAQDQGQSLKTRTMLQADINRLMEELDNIANTT 129
          ALGILQTADKAMDEQLKILDITIKTKATQAAQDQGQSLKTRTMLQADIN+LMEELDNIANTT
Sbjct: 61  ALGILQTADKAMDEQLKILDITIKTKATQAAQDQGQSLKTRTMLQADINKLMEELDNIANTT 120

Query: 130 SFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSFSSTVGLTI 189
          SFNGKQLLSGGFTNQEFQIGSSSNQT+KA+IGATQSSKIGVTRFETGSQSFS+SG VGLTI
Sbjct: 121 SFNGKQLLSGGFTNQEFQIGSSSNQTVKATIGATQSSKIGVTRFETGSQSFTSGIVGLTI 180

Query: 190 KNYNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDVKSVGAYAIKAGNTS 249
          KNYNGIEDFKFD+VVISTSVGTGLGALAEIN+NADKTG+RAT+DVK+ GAYAIKAG TS
Sbjct: 181 KNYNGIEDFKFDNVVISTSVGTGLGALAEINKNADKTGVRATYDVKTTGAYAIKAGTTS 240

Query: 250 QDFAINGVVIGKVDYSDGDENGSLISAINAVKDDTTGVQASKDENGKLVLTSAADGRGIKIT 309
          QDFAINGV+IGKVDY DGD NGSLISAINAVKDDTTGVQASKDENGKLVLTSAADGRGIKIT
Sbjct: 241 QDFAINGV+IGKVDYKDGDNNGSLISAINAVKDDTTGVQASKDENGKLVLTSAADGRGIKIT 300

```